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October 26, 2004, 15:19:44; Search time 44.6154 Seconds (without alignments) 64.324 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match .0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	Abg65707 Plant ICK		Plant	Rice	Rice	Maize	2 Maize	245 Corn	940	4 Corn	250 Corn	249 Corn	2 Rice		_	Abg65701 Plant ICK	_	0		Abg69080 Botulinum	_	<u>ж</u>	Clost	59	1734
SUMMARIES	ID	ABG65707	ABG65702	ABG65706	195	5	S	ABB98862	AAB26245	AAP01940	ABG65674	AAB26250	AAB26249	ABG65692	ABB98757	ABG65670	ABG65701	AAB27259	AAY44340	AAE25108	ABG69080	ABG69070	ABG69081	ADN11038	ABR53595	ADK64734
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RESU ABG6	
O X	ABG65707 standard; peptide; 8 AA.
AC	ABG65707;
X E	27-AUG-2002 (first entry)
S X	Plant ICK protein conserved motif 1 #15.
XX	Plant; inhibitor of cyclin dependent kinase; ICK.
×	
SO	Zea mays.
X	
Nd	WO200228893-A2.
×	
50	11-APR-2002.
×	
단	29-JUN-2001; 2001WO-IB001492.
X	
PR	14-JUL-2000; 2000US-0218471P.
PR	
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PA	(CROP-) CROPDESIGN NV.
×	
Ιđ	Frankard VMS, Peres Bota AM, Droual A, Mironov V,
БI	Hatzfeld Y;
X	
מ	WBT: 2002-471311/50.

Ω Inze WPI; 2002-471311/50.

Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors. Disclosure; Page 14; 141pp; English.

This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by this fiftent or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to ICK protein, forms which have decreased or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention

Plant; inhibitor of cyclin dependent kinase; ICK.

Plant ICK protein conserved motif 1 #14

27-AUG-2002

ABG65706;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.
                                               Gaps
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0
                     Score 36; DB 5; Length 8;
Pred. No. 1.7e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 5; Length 8; Pred. No. 1.7e+06; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Droual A, Mironov V,
                                                                                                                                                                                                                                 Plant; inhibitor of cyclin dependent kinase; ICK.
                                                                                                                                                                                                             Plant ICK protein conserved motif 1 #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14; 141pp; English.
                                                                                                                                            ABG65702 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Frankard VMS, Peres Bota AM,
Hatzfeld Y;
                      94.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                         29-JUN-2001; 2001WO-IB001492
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13-OCT-2000; 2000US-0241219P.
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                         (first entry)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                (CROP-) CROPDESIGN NV
                                                                α
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                  Query Match
Best Local Similarity
                                                                1 FXXKYNFD
                                                                                       FASKYNFD
                                                                                                                                                                                                                                                                             WO200228893-A2
Sequence 8 AA;
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                                                                                                                                                                                                                                                          Oryza sativa.
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                                                                                                                                                                                        27-AUG-2002
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                                                                                                                                                                   ABG65702;
                                          Matches
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Matches
                                                                                                                      RESULT 2
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Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production

Disclosure, Page 14; 141pp; English

inhibitors.

ICK

â Inze

Mironov V,

Droual A,

Peres Bota AM,

Frankard VMS, Hatzfeld Y;

WPI; 2002-471311/50.

(CROP-) CROPDESIGN NV

29-JUN-2001; 2001WO-IB001492. 14-JUL-2000; 2000US-0218471P.

WO200228893-A2.

11-APR-2002

Oryza sativa,

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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of ICK inhibitors of cyclin Dependent Kinases) proteins. The sequences of insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to ICK protein, forms which have decreased or aberrant activity compared to ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice; plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice Cyclin dependent kinase inhibitor (CDKI) clone rds2c.pk0088.024.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                    94.7%; Score 36; DB 5; Length 8; 75.0%; Pred. No. 1.7e+06; ive 0; Mismatches 2; Indels
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Misc-difference 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP01950 standard; protein; 37 AA.
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                                                                                                                                                                                                                                                                                                         Similarity
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Best Local S
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Gaps

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ABG65706 standard; peptide; 8 AA.

RESULT 3 ABG65706 ID ABG6

FXXKYNFD 8 FAAKYNFD 8

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ABB98860;
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ABB98860
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                                                                                                                                                                                                                 The invention describes a novel isolated polynuclectide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequence is the rice CDKI clone rds2c.pk008.024 as described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division; cell growth; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                  Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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Mismatches
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/note= "Encoded by GTCA"
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Pred. No.
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                                                                                                                                                                                                  Claim 10; Fig 1; 58pp; English
                                                                                                                    Cahoon RE;
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                                                                                                (DUPO ) DU PONT DE NEMOURS' &
                                                                                                                                                                                                                                                                                                                                                                                 94.78;
75.08;
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                                                         06-APR-2000; 2000WO-US009106
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                                                                                                                                      WPI; 2000-679375/66.
                                                                                                                   Weng Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                          FXXKYNFD
                                                                                                                                                  N-PSDB; AAN02400
                                                                                                                                                                                                                                                                                                                                                               Sequence 37 AA;
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                  WO200060087-A2
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Best Local (
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                                                                                                                                                                                                                                               The present sequence is the rice cyclin-dependent kinase inhibitor (CDKI). Its coding sequence was isolated by searching a rice seed cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in other organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel cyclin-dependent kinase polymucleotides and their encoded proteins, involved in cell cycle regulation, and useful for altering cell cycle protein content, cell cycle progression, cell number and composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to maize cyclin-dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize, cyclin-dependent kinase inhibitor; CKI; plant, corn, crop yield; root size, plant growth; tassel size, ear size, male sterility; endoreduplication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                  Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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Pred. No. 2.1;
); Mismatches
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                Ξ.
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ARIZONA BOARD OF REGENTS.
                (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB98860 standard; protein; 42
                                                                                                                                                                                                                   Claim 10; Fig 1; 58pp; English
                                                         Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                             WPI; 2000-679375/66.
N-PSDB; AAA95286.
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                                                         Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FXXKYNFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37 AA;
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                                                         Klein TM,
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CC (CKI), CKI B, CKI C and CKI D. The coding sequences (I) for these proteins are useful for modulating the activity of CDK in a plant such as a corn, soybean, sunidower, sorghum, canola, wheat, alfalfa, cotton, crice, barley, oil-seed Brassica and millet. Modulating the activity of growth in a plant, especially a positive growth advantage and modulating CDK activity upward is useful for increasing crop yield, root size, plant growth, tassel size and/or ear size. Modulating CDK activity is also conserui for conferring male sterility and for improving transformation frequencies by increasing the number of cells in cell division. CDK activity can also be modulated for modulating endoreduplication in the conferring male sterility and for improving transformation frequencies by increasing the number of cells in cell division. CDK activity can also be modulated for modulating endoreduplication in the condonated in one or more tissues of a plant, comprising root, seed, cassel, earls, embryo, flower, grain, germ, head, leaves, tassel, ear, salk, stark, embryo, flower, grain, germ, head, leaves, stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm, pericarp, meristematic or leaf cells. (I) is also useful for identifying contines, ear, salk stark, embryo, flower, grain, germ, head, leaves, stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm, ce a second nucleic acid sequence encoding a DNA-binding domain. The present contains a CDK binding region and/or cyclin binding domains

Sequence 42 AA;

ö Score 36; DB 6; Length 42; Pred. No. 2.4; 0; Mismatches 2; Indels 94.7%; Query Match Best Local Similarity 75.0%; Tranes 6; Conservative ω 1 FXXKYNFD ò g

14 FASKYNFD 21

ABB98862 standard; protein; 46 AA. ABB98862;

(first entry) 21-FEB-2003

Maize CKI_D C-terminal protein fragment.

Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield; root size; plant growth; tassel size; ear size; male sterility; endoreduplication.

Zea mays.

WO200281623-A2.

17-OCT-2002.

07-NOV-2000; 2000US-0246349P. D6-NOV-2001; 2001WO-US044038.

(PION-) PIONEER HI-BRED INT INC

(ARIZ-) ARIZONA BOARD OF REGENTS.

BR, Dilkes Larkins BA, Lowe KS, WPI; 2003-058511/05. 3ordon-Kamm WJ,

Novel cyclin-dependent kinase polymucleotides and their encoded proteins, involved in cell cycle regulation, and useful for altering cell cycle protein content, cell cycle progression, cell number and composition of

Example 11; Page 46; 69pp; English

plants,

The present invention relates to maize cyclin-dependent kinase inhibitor (CKI), CKI_B, CKI_C and CKI_D. The coding sequences (I) for these

con, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed Brassica and millet. Modulating the activity of cotton, soybean, soundating downward is useful for providing differential growth in a plant, especially a positive growth advantage and modulating growth in a plant, especially a positive growth advantage and modulating cot of activity upward is useful for increasing crop yield, root size, plant growth, tassel size and/or ear size. Modulating CDK activity is also useful for conferring male sterility and for improving transformation frequencies by increasing the number of cells in cell division. CDK cativity can also be modulated for modulating endoreduplication in the cativity can also be modulated for modulating endoreduplication in the chooser used is an endospermerpreferred promoter. The cell numbers are modulated in one or more tissues of a plant, comprising root, seed, tassel, ear silk, stalk, embryo, flower, grain, germ, head, leaves, pericarp, meristematic or leaf cells (i) is also useful for identifying maize CKI interacting proteins, by adducting the nucleic acid sequence to a sequence is a C-terminal protein fragment of CKI D. This sequence proteins are useful for modulating the activity of CDK in a plant such as

Sequence 46 AA;

Gaps .; 0 Length 46; 2; Indels 9 94.7%; Score 36; DB 6 75.0%; Pred. No. 2.6; ive 0; Mismarches Query Match Best Local Similarity 75.v. Sinana 6; Conservative

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ò g AAB26245

AAB26245 standard; protein; 53 AA.

AAB26245;

(first entry) 17-JAN-2001

Corn cyclin-dependent kinase inhibitor #1.

Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division; cell growth; herbicide.

Zea mays.

WO200060087-A2.

12-OCT-2000.

06-APR-2000; 2000WO-US009106.

07-APR-1999; 99US-0128192P.

(DUPO) DU PONT DE NEMOURS & CO

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Klein TM, Weng Z, Cahoon RE;

WPI; 2000-679375/66.

N-PSDB; AAA95276.

Cyclin dependent kinase inhibitor sequences, useful for identifying nerbicides and plant growth inhibitors.

Claim 10; Page 40; 58pp; English.

The present sequence is the corn cyclin-dependent kinase inhibitor (CDKI). Its coding sequence was isolated by searching a corn silk cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of

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RESULT 10
ABG65674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a novel isolated polynuclectide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the corn CDKI clone csiln.pk0050.e6 as described
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transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in other organisms
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; corn; plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                            Corn Cyclin dependent kinase inhibitor (CDKI) clone csiln.pk0050.e6
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                                                                                              Length 53;
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                                                                                              Score 36; DB 3;
Pred. No. 3;
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Pred. No.
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                                                                                                                                                                                                                                                                            AAP01940 standard; protein; 53 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2000; 2000WO-US009106.
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75.0%;
                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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in the method of the i
                                                                                                                                                                                           30 FASKYNFD 37
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Best Local Similarity
Matches 6; Conserv
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                                                                   Sequence 53 AA;
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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity, compared to ICK wild type protein. The present sequence represents an inhibitor of AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
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                                                                                                                                                                                Plant; inhibitor of cyclin dependent kinase; ICK.
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Pred. No.
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ABG65674 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 48; Fig 4; 141pp; English.
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2000US-0241219F.
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Best Local Similarity
                                                                                                                                           Corn ICK 1 protein.
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Hatzfeld Y;
                                                                                                                                                                                                                                                                                                                                                                                         14-JUL-2000;
13-OCT-2000;
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27-AUG-2002
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                                       ABG65674;
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FXXKYNFD 8

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Zea mays

Klein TM,

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The present sequence is the corn cyclin-dependent kinase inhibitor (CDKI). Its coding sequence was isolated by searching a corn silk cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in other organisms
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                                                                                                 Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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Pred. No. 7.7;
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Cahoon RE
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Hatzfeld Y;
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75.0%;
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2000US-0241219P.
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N-PSDB; ABK93981.
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Best Local Similarity
Matches 6; Conserv
Weng Z,
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                                                          N-PSDB; AAA95280
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 126 AA;
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13-OCT-2000;
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Klein TM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the corn cyclin-dependent kinase inhibitor (CDKI). Its coding sequence was isolated by searching a contig comprising cDNA from corn roots and ear leaf sheath for sequences similar to those encoding the CDKI from Chenopolium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of the protein decreased in genetic and physical mapping and in the isolation of the
            Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division; cell growth; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn, cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division; cell growth; herbicide.
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                                                                                                                                                                                                                                                                                                                           Cahoon RE;
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N-PSDB; AAA95281.
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Matches 6; Conserv
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Query Match

AAB26249;

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Gaps

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Length 126; Indels us-09-574-735c-34.rag

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The present sequence is maize cyclin-dependent kinase inhibitor (CKI), CKI B. The coding sequence for this protein (1) is useful for modulating solventy of cyclin-dependent kinase (CMK) in a plant such as a corn, soybean, sunflower, sorghum, cannol, wheat, alfalfa, cotton, rice, barley, oil-seed Brassica and millet. Modulating the activity of CDK, preferably modulating downward is useful for providing differential growth in a plant, especially a positive growth advantage and modulating CDK activity upward is useful for increasing crop yield, root size, plant growth, tassel size and/or ear size. Modulating CDK activity is also useful for conferring male sterility and for improving transformation frequencies by increasing the number of cells in cell division. CDK activity can also be modulated for modulating endoreduplication in the
                                                                                                                                                                                        ö
the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel cyclin-dependent kinase polynucleotides and their encoded proteins, involved in cell cycle regulation, and useful for altering cell cycle protein content, cell cycle progression, cell number and composition of
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize; cyclin-dependent kinase inhibitor; CKI; CKI B; plant; corn; crop yield; root size; plant growth; tassel size; ear size; male sterility; endoreduplication.
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                                                                                                                                                        5,
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Pred. No. 14;
0; Mismatches
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/note= "Conserved domain"
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                                                                                                                                                                                                                                                                                                                                           ABB98757 standard; protein; 256 AA.
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                                                                                                                                                    94.7%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                         196 FAAKYNFD 203
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N-PSDB; ABV74603.
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                                                                                                                        Sequence 226 AA;
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(ARIZ-) ARIZONA
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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
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endosperm of corn, sorghum, wheat, rice, barley, and millet, where the promoter used is an endosperm-preferred promoter. The cell numbers are modilated in one or more tissues of a plant, comprising root, seed, tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves, stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm, pericarp, meristematic or leaf cells. (I) is also useful for identifying maize CKI interacting proteins, by adducting the nucleic acid sequence to a second nucleic acid sequence encoding a DNA-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used tro screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.
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Pred. No. 16;
0; Mismatches
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                      ABG65670 standard; protein; 262 AA
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                                                                                                                                                                             94.7%;
75.0%;
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13-OCT-2000; 2000US-0241219P.
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75.0%;
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                           1 FXXKYNFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; inhibitor
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                                                                                                                                                 Sequence 256 AA;
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Matches
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ABG65670
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2; Indels 0; Mismatches Matches 6; Conservative

1 FXXKYNFD 8 | | | | | | | | 233 FAAKYNFD 240

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Search completed: October 26, 2004, 15:36:51 Job time: 45.6154 secs

Sequence 51, Appl Sequence 49; Appl Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequ

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Sequence 6, Application US/09526597D
; Sequence 6, Application US/09526597D
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: Landrieu, Jaheile
; APPLICANT: Landrieu, Jaheile
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION WUBBR: US/09/526,597D
; CURRENT APPLICATION WUBBR: US/09/526,597D
; CURRENT PILING DATE: 2000-03-16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH 223
                                                                                                                                                                                                                                                                         RESULT 1
US-09-526-597D-4
US-09-526-597D-4
Sequence 4, Application US/09526597D
Sequence 7, Application US/09526597D
Sequence 7, Application US/09526597D
September 100:
APPLICANT: De Veylder, Lieven
APPLICANT: De Almeida, Janice
APPLICANT: Landrieu, Isabelle
TITLE OF INVENTION CYCLIN-dependent kinase inhibitors and uses thereof
CURRENT APPLICATION NUMBER: US/09/526,597D
CURRENT APPLICATION NUMBER: US/09/526,597D
CURRENT APPLICATION NUMBER: US/09/526,597D
CURRENT FILING DATE: 2000-03-16
NUMBER: OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 4; Length 223;
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Pred. No. 9.2;
0; Mismatches 2; Indels
US-08-455-543A-51

US-08-23-305C-49

US-08-23-305C-49

US-08-311-33-2

US-09-315-51-2

US-09-315-51-4

US-09-315-51-4

US-09-315-51-4

US-09-315-51-4

US-09-315-51-4

US-09-315-51-4

US-09-316-51-4

US-09-31-41-4

US-09-31-41-4

US-09-31-41-4

US-09-31-41-4

US-09-31-41-4

US-09-31-41-4

US-09-164-615-5

US-09-164-615-5

US-09-039-198A-15

US-09-039-198A-15

US-09-039-188A-15

US-09-039-188A-15

US-09-039-188A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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22175
22373
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2216
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3733
3733
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 US-09-526-597D-4
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LENGTH: 222
   Query Match
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Sequence 1835, A
Sequence 1831, A
Sequence 16531, A
Sequence 516, App
Sequence 42, App
Sequence 42, App
Sequence 4019, A
Sequence 4019, A
Sequence 49236, A
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds (without alignments) 40.099 Million cell updates/sec
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Sequence 7, A
Sequence 45,
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Sequence 2, A
Sequence 49,
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Sequence 7, A
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                                                                                                                                                                                                                                                                                                                                               lssued Patents AA:*
1. /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
7: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
7: /cgn2 6/ptodata/1/iaa/Packfiles1.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-526-597D-6
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US-09-248-796A-16581
US-09-248-796A-16581
US-09-270-767-34252
US-09-270-767-34252
US-09-270-767-34019
US-09-270-767-4469
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US-09-295-541-5
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US-09-395-541-5
US-09-395-541-5
US-09-395-744-6
US-09-395-744-6
US-09-495-714C-4
US-08-495-714C-4
US-08-495-714C-6
US-08-455-206A-7
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                                                                                                                                                                                                                      478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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1 FXXKYNFD 8
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Match Length
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Perfect score:
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GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
FILE REFERENCE: 1596-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 0/127,352
PRIOR PLICATION NUMBER: 60/127,352
PRIOR PLING DATE: 1990-04-01
PRIOR PLING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1387
SOUTHARE: CURAPARSEGFORMATTER VERSION 0.9
SOUTHARE: CURAPARSEGFORMATTER VERSION 0.9
SEQ ID NO 536
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APPLICANT: Doran, James L.
APPLICANT: Callinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 4; Length 648;
Pred. No. 1.2e+02;
1; Mismatches 2; Indels
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in LOCATION: (0)...(0)
cother Indexation: Polypeptide Accession Number YLR098C
US-09-538-092-536
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COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC CAPACTERISTICS:
COMPUTER: 
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6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
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Best Local Similarity 62.5%;
Matches 5; Conservative
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US-09-248-796A-18335

Sequence 18335 Application US/09248796A

TITLE OF INVENTION: VOLCEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-06-13

NUMBER: OF SEQ ID NOS: 28208

SEQ ID NO 18335

LENGTH: 118
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Separation US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

TITLE OF INVENTION:

FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PILLOR DATE: 1999-02-12

CURRENT PILLOR DATE: 1999-02-12

PRIOR FILLOR DATE: 1998-02-13

PRIOR FILLOR DATE: 1998-02-13

PRIOR FILLOR DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16581

LENGTH: 385
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Pred. No. 20;
1; Mismatches 2; Indels
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Pred. No. 69;
1; Mismatches 2; Indels
                                      2; Indels
      Pred. No. 9.2;
0; Mismatches
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US-09-538-092-536
; Sequence 536, Application US/09538092
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62.5%;
   75.0%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
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US-09-248-796A-18335
Best Local Similarity 75.0
Matches 6; Conservative
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; ORGANISM: Candida albicans
US-09-248-796A-16581
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Best Local Similarity 62.5
Matches 5, Conservative
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US-09-248-796A-16581
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Sequence 49236, Application US/09270767
Parent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REPERBNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILMS DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
TITLE OF INVENTION NUMBER: 08/09/270,767
CURRENT APPLICATION NUMBER: 08/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47469
LENGTH: 147
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100.0%; Pred. No. 48;
iive 0; Mismatches
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                                                                                                                                                                                                                                                        78.9%; Score 30; DB 100.0%; Pred. No. 41; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-34019
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ORGANISM: Drosophila melanogaster
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-270-767-49236
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LENGTH: 170
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LENGTH: 170
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOMOLOGY et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFFWARE: Referent Ver. 2.0
SEQ ID NO 32222
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERBNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PARENTIN VET. 2.0
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100.0%; Pred. No. 23;
tive 0; Mismatches
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Parent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
                                                                                                                                                                                                                                                                                                                       Sequence 61052, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Drosophila melanogaster US-09-270-767-61052

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32252

                                                                                           81.6%;
62.5%;
                                                                                        Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-233-788A-42
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Best Local Similarity
Matches 5; Conserv
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US-09-270-767-47469
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US-09-270-767-32252
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US-09-270-767-61052
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LENGTH: 85
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45543
LENGTH: 363
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Best Local Similarity
Matches 5; Conserv
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Sequence 7509, Application US/09328352

Sequence 7509, Application US/09328352

Sequence 7509, Application US/09328352

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 348
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                         Sequence 2, Application US/09526597D

Patent No. 6710227

Batent No. 6710227

Batent No. 6710227

APPLICANT: De Veylder, Lieven

APPLICANT: De Almeida, Janice

APPLICANT: De Almeida, Janice

APPLICANT: Landrieu, Isabelle

TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

FILE REFERENCE: 1187-2

CURRENT PRILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 209
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-7509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-2
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                103 KYNFD 107
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                           4 KYNFD 8
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US-09-270-767-45543
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US-09-526-597D-2
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PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR PARTE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/241,219
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: S9
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
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                                                                                                                                                                                                                                   October 26, 2004, 15:19:44 ; Search time 115.077 Seconds (without alignments) 22.507 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/DEC_NEW_PUB_PEP:*

3: /cgn2_6/ptodata/2/pubpaa/USO_NEW_PUB_PEP:*

4: /cgn2_6/ptodata/2/pubpaa/USO_NEW_PUB_PEP:*

5: /cgn2_6/ptodata/2/pubpaa/USO_NEW_PUB_PEP:*

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8: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB_PEP:*

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11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_PEP:*

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13: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_PEP:*

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16: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_PEP:*

17: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_PEP:*

18: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_PEP:*

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10: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_PEP:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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38
1 FXXKYNFD 8
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Maximum DB seg length: 200000000
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Perfect score:
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SUMMARIES

		æ					
Result		Query					
No.	Score	Match	Match Length DB	DB	ID	Description	
	36	94.7	116	15	US-10-333-006-14	Sequence 14, Appl	
2	36	94.7	221	15	US-10-425-114-69245	Sequence 69245, A	
ო	36	94.7		15	US-10-333-006-55	Sequence 55, Appl	
4	36	94.7		σ	US-09-993-308-2	Sequence 2, Appli	
S	36	94.7		11	US-09-993-808B-2	Sequence 2, Appli	
9	36	94.7		15	US-10-333-006-10	Sequence 10, Appl	
7	36	94.7		15	US-10-425-114-63204	Sequence 63204, A	
80	36	94.7		16	US-10-437-963-122432	Sequence 122432;	
6	36	94.7		16	US-10-437-963-195115	Sequence 195115,	
10	36	94.7		16	US-10-437-963-122443	Sequence 122443,	
11	35	92.1		75	US-10-424-599-212181	Sequence 212181,	
12	35	92.1		9	US-09-733-507-16	Sequence 16, Appl	
13	35	92.1		15	US-10-451-139-15	Sequence 15, Appl	

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Gaps

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Query Match 94.7%; Score 36; DB 15; Length 116; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 0; Mismatches 2; Indels

LOCATION: (11) (11) (11) COTHER INFORMATION: Xaa = any amino acid US-10-333-006-14

FEATURE:
NAME/KEY: misc_feature TYPE: PRT ORGANISM: Zea mays LENGTH: 116

ednence ednence ednence ednence ednence ednence ednence ednence	sequence 168, Appsequence 66, Appls Sequence 66, Appls Sequence 165, Appls Sequence 125, Appls Sequence 13, Appls Sequence 13, Appls Sequence 14, Appls Sequence 14, Appls Sequence 24, Appls Sequence 10, Appls Sequence 12, Appls Sequence 11,	Allle S. ASE INHIBITORS
9 99997	US-10-452-024-168 US-10-729-122-66 US-10-729-122-66 US-10-452-024-165 US-10-452-024-165 US-10-452-024-165 US-10-369-493-22428 US-10-313-006-13 US-10-313-006-13 US-10-313-006-13 US-10-313-006-13 US-10-313-006-13 US-10-313-006-13 US-10-99-138-14 US-09-99-188B-4 US-09-99-188B-4 US-09-733-507-10 US-09-733-507-10 US-10-451-139-12 US-10-451-139-12 US-10-451-139-12 US-10-451-139-12 US-10-451-139-12	ALIGNMENTS 14, Application US/10333006 16n No US20040019926A1 11NPORMATION: WI: Frankard, Valerie Marie-No. US20040019926A1111 WI: Frankard, Valerie Maries WI: Droual, Anne-Marie WI: Inz, Dirk WI: Inz, Dirk WI: Hatzfeld, Yves FRINGNIS NOVEL PLANT CYCLIN-DEPENDENT KINASE REREALS 1187-13 APPLICATION NUMBER: US/10/333,006 FILING DATE: 2003-01-14 ILING DATE: 2001-06-29
0 1 4 4 5 5 6 6 6 7 4 4 4 1 1 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1		US/10333 19926A1 19926A1 lerie Mar Adrian P Adri
4 4 8 4 1 1 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4	00000000000000000000000000000000000000	cation US/10 20040019926A Td, Valerie Bota, Adria: I, Anne-Maria: V, Vladimir Dirk Dirk N: NOVEL PLAI 187-13 DN NUMBER: U NU
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Lowe, Keith S.
APPLICANT: Larkins, Brian A.
APPLICANT: Larkins, Brian A.
APPLICANT: Larkins, Brian R.
APPLICANT: Dilkes, Brian R.
APPLICANT: Dilkes, Brian R.
APPLICANT: Sun, Yuejin
TITLE OF INVERMION: Cell Cycle Nucleic Acide, Polypeptides and Uses Thereof CURRENT APPLICATION NUMBER: US/09/993,308
CURRENT APPLICATION NUMBER: 60/246,349
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 6
SOFTHARE: Patentin version 3.1
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09993808B

Sequence 2, Application US/09993808B

Bublication No. US20040003433A1

GENERAL INFORMATION:
APPLICANT: Gordon-Kamm, William
APPLICANT: Sun, Yuejin
APPLICANT: Dixes, Brian
APPLICANT: Larkins, Brian
APPLICANT: Larkin
                                                                94.7%; Score 36; DB 15; Length 226; 75.0%; Pred. No. 23; 23; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 256; 26;
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Pred. No. 26;
0; Mismatches 2; Indels
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Pred. No.
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COTHER INFORMATION: Xaa = Any Amino Acid
US-09-993-808B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09993308 Patent No. US20020159435A1
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75.0%;
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                                      Query Match
Best Local Similarity 75...
-Loc 6; Conservative
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Best Local Similarity 75.00
Thes 6; Conservative
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Best Local Similarity
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ORGANISM: zea mays
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Zea mays
US-09-993-308-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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JS-10-333-006-55
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Publication No. US20040019926A1

Publication No. US20040019926A1

SEQUENCE INFORMATION:
APPLICANT: Prankard, Valerie Marius
APPLICANT: Proual, Anne-Marie
APPLICANT: Mironov, Vladimir
APPLICANT: Mironov, Vladimir
APPLICANT: Mironov, Vladimir
APPLICANT: Mironov, Vladimir
APPLICANT: Harzfeld, Yves
IIIZ, Dirk
APPLICANT: Harzfeld, 1000
IIIZ, Dirk
APPLICANT: Harzfeld, 1000
IIIZ, Dirk
APPLICANT: Harzfeld, 1000
IIIZ, PRINKENTION: UNMBER: US/10/333,006
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR PILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CTHER INFORMATION: Clone ID: LIB3079-036-F9_FLI.pep
US-10-425-114-69245
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LOCATION: (119)..(119)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                       Sequence 69245, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: probe or primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                          89 FASKYNFD 96
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                                      1 FXXKYNFD 8
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FEATURE:
                                                                                                                                                                                                                                                                                        -10-425-114-69245
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APPLICANT: La Noval, Thomas J.
APPLICANT: Sovalic, David K.
APPLICANT: Storaic, David K.
APPLICANT: Storaic, David K.
APPLICANT: Storaic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wai wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(5321)
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 195115
LENGTH: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
SEQ ID NOS: 204966
SEQ ID NO 122432
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Pred. No. 35;
0; Mismatches 2; Indels
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US-10-437-963-122432
                                                                                                                                                                                                          Sequence 122432, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J.; APPLICANT: Kovalic, David K.; APPLICANT: Toou, Yihua APPLICANT: Toou, Yonwei; APPLICANT: Wu, Weisharov, Andrey A.; APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 195115, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 75.0°
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
                                                                      235 FASKYNFD 242
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Matches 6; Conserva
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19.56quence 10, Application US/10333006

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26;
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Indels
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; CTHER INFORMATION: Clone ID: UC-ZMFLMO17355F05_F1I.pep.US-10-425-114-63204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1
Pred. No. 26;
0; Mismatches
Mismatches
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SOFWARE: Patentin version 3.1
SEQ ID NO L
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
6; Conservative
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GORGANISM: Oryza sativa
US-10-333-006-10
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                                                                                                    228 FASKYNFD 235
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ORGANISM: Zea mays
Matches
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RESULT 12
US-09-733-507-16
is agguence 16, Application US/09733507
patent No. US20010025379A1
patent No. US20011 No. Regulators
patent No. UNENTION: Regulators
patent APPLICATION NUMBER: US/09/733,507
patent Patent APPLICATION NUMBER: CA 2,256,121
patent NUMBER OF SEQ ID NOS: 16
patent No. 16
patent No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | APPLICANT: WANG, HONG
| APPLICANT: WANG, HONG
| APPLICANT: ZHOU, YONGMING
| APPLICANT: ZHOU, YONGMING
| APPLICANT: ZHOU, YONGMING
| APPLICANT: FOWKE, LARRY C.
| APPLICANT: FOWKE, LARRY C.
| APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF APPLICANT: HER MAJESTY IN RIGHT OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR ITLE OF INVENTION: MODILATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR | TILLE OF INVENTION: MODILATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR |
| FILE REPERENCE: 4810-62237 |
| CURRENT FILING DATE: 2003-06-18 |
| FRIOR PILING DATE: 2001-12-18 |
| FRIOR PILING DATE: 2001-12-18 |
| FRIOR PILING DATE: 2000-12-18 |
| NUMBER OF SEQ ID NOS: 23 |
| SOFTWARE: PATENTING DATE: 2006-26-18 |
| LENGTH: 196 |
| TYPE: PRT |
| CORGANISM: Chenopodium rubrum |
| TYPE: PRT |
| CORGANISM: Chenopodium rubrum |
| TYPE: PRT |
| CORGANISM: Chenopodium rubrum |
| CORGANISM: CHENCE |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 75.0%; Pred. No. 31; 6; Conservative 0; Mismatches 2; Indels
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US-10-011-588-31
Sequence 31, Application US/10011588; Publication No. US20020168727A1; GENERAL INFORMATION:
APPLICANT: Smith, Leonard; APPLICANT: Jensen, Melody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/10451139 Publication No. US20040098763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Chenopodium rubrum
US-09-733-507-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Chenopodium rubrum
US-10-451-139-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 FSEKYNFD 178
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Best Local Similarity
Matches 6; Conserv
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; Publication No. US2004012334341
; GENERAL INPORMATION:
   APPLICANT: La Rosa, Thomas J.
   APPLICANT: Covalic, David K.
   APPLICANT: Zhou, Yihua
   APPLICANT: Alou, Yihua
   APPLICANT: Alou, Yihua
   APPLICANT: Boukharov, Andrey A.
   APPLICANT: Boukharov, Andrey A.
   APPLICANT: Boukharov, Andrey A.
   APPLICANT: Brand David K.
   APPLICANT: Brand Use Andrey A.
   APPLICANT: Brand Use Andrey A.
   APPLICANT: Brand Use Thereof for Plant Improvement
   FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
   FILE REFERENCE: 38-21(53221)
   CURRENT APPLICATION NUMBER: US/10/437,963
   CURRENT FILING DATE: 2003-05-14
   NUMBER OF SEQ ID NOS: 204966
   SEQ ID NO 122443
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Sequence 212181, Application Wolf US/204031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENGTH: 176

LENGTH: 176

LENGTH: 176
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US-10-424-599-212181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2536C.1.pep
US-10-437-963-122443
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                 388 FAAKYNFD 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 FAAKYNFD 239
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                 1 FXXKYNFD 8
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US-10-437-963-122443
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Sequence II, Application US/10011588

Publication No. US2020168727A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Smith, Leonard

APPLICANT: Smith, LoghT CHAINS OF BOTULINUM

TITLE OF INVENTION: RECEMBINANT LIGHT CHAIN FUSION PROTEINS FOR USE IN

TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY

FILE REFERENCE: A34796 667252.0113

CURRENT APPLICATION NUMBER: 2002-03-29

PRIOR APPLICATION NUMBER: 60/246,744

PRIOR PELING DATE: 2000-07-06

PRIOR APPLICATION NUMBER: 60/246,744

PRIOR APPLICATION NUMBER: 60/246,744

PRIOR APPLICATION NUMBER: 60/246,744

PRIOR APPLICATION NUMBER: 60/246,744

PRIOR PILING DATE: 2000-01-06

PRIOR APPLICATION NUMBER: 60/246,744

PRIOR PILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

TWOEL DATE:

TWOEL DATE:

LENGTH: 441
TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
TITLE OF INVENTION: RECEMBERAND LIGHT CHAIN FUSION PROTEINS FOR USE IN
TITLE OF INVENTION: RESERRER AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
FILE REFERENCE: A34796 067252.0113
CURRENT APPLICATION NUMBER: US/10/011,588
FRIOR PELING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 09/910,186
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR APPLICATION NUMBER: 60/246,744
PRIOR APPLICATION NUMBER: 60/246,744
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 47
COSTWARE FASTESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.1%; Score 35; DB 13; Length 440; Best Local Similarity 75.0%; Pred. No. 69; Matches 6; Conservative 0; Mismatches 2; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 FSEKYNFD 331
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US-10-011-588-31
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LENGTH: 440
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325 FSEKYNFD 332

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Search completed: October 26, 2004, 15:33:29
Job time: 116.077 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 26, 2004, 15:27:13 ; Search time 11.0769 Seconds (without alignments) 69.490 Million cell updates/sec Run on:

US-09-574-735C-34 38 1 FXXKYNFD 8 Title: Perfect score: Sequence: BLCSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 79:*
1: Dirl:*
2: DirZ:*
3: DirZ:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	cyclin-dependent k	ntrC family transc	botulinum neurotox	botulinum neurotox	DNA-directed RNA p	cyclin-dependent k	chitinase (EC 3.2.	chitinase (EC 3.2.	٠ -	1-like r		hypothetical prote	-COA	transcription acti	ы	mbran	cal	ical	ical	a]	al	a]	ä	Ų	etic	der	ellar	aprenyl	aprenyl
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d	Query Match	. ^1	ÀΙ	92.1	\sim 1	\sim	CD	(T)	n	₹#	-			-1	-	_		_	(D)	œ	CD)	CO)	œ	CD)	œ	œ	œ	œ	œ	œ
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	Result No.		N	м	4	Ŋ	9	7	∞	σ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

probable N-acetyl- D-2-hydroxy-acid d	probable exported hypothetical prote hypothetical prote	secretory protein hypothetical prote trigger factor 2 (translation elonga hypothetical prote trigger factor tig	xylulokinase homol phenylalanine-tRNA	hypotherical prote NADH2 dehydrogenas
C71180 F64047	A10284 T33906 E90099	S27879 T18813 I40755	S72277 AE2163 H81437	E69895 T28752	1003413 H84957 S44478
330 2	334 345 365 2	399 2 408 2 410 1	410 2 413 2 444 2	552 2	617 2 644 2
78.9	78.9 78.9	78.9 78.9 9.9	78.9 78.9	78.9	78.0
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30	3 3 3 3 8 4	35 36 37	8 6 0 8 6 0	44.	4 4 4 2 4 2

ALIGNMENTS

RESULT 1 10996a cyclin-dependent kinase inhibitor protein - red goosefoot C;Species: Chenopodium rubrum (red goosefoot) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change

09-Jul-2004

C;Accession: T0968
R;Fountain, M.D.; Renz, A.; Beck, E.
submitted to the EMBL Data Library, November 1997
A;Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophi, A;Peference number: Z16910
A;Accession: T09968
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T09968
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosiques: 1-196 <FQUI>A;Accession: T09968
A;Experimental type: mRNA
A;Experimental source: photoautotrophic cells derived from hypocotyl tissue
C;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: protein kinase inhibitor

ó Gaps .. Query Match

92.1%; Score 35; DB 2; Length 196;
Best Local Similarity 75.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 2; Indels

171 FSEKYNFD 178 1 FXXKYNFD 8 g à

RESULT 2

The family transcription regulator (PAS and AAA domains) [imported] - Clostridium aceturic formity transcription regulator (PAS and AAA domains) [imported] - Clostridium acetobutylicum c; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (Accession: D6956 (Accession: D6956

A;Cross_references: UNIPROT:097LU5; GB:AE001437; PIDN:AAK78439.1; PID:g15023316; GSPDB: A;Experimental source: Clostridium acetobutylicum ATCC824

A; Gene: CAC0459

. 0 Query Match 92.1%; Score 35; DB 2; Length 627; Best Local Similarity 75.0%; Pred. No. 13; Matches 6; Conservative 0; Mismatches 2; Indels

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Gaps

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cyclin-dependent kinase inhibitor protein [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein F2686.8
C.Species: Arabidopsis thaliana (mouse-ear cress)
R.Rounsley, S.D.; Kaul, S.; Lin, X.; Retchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the RMEL Data Library, June 1998
A.Reference number: Z14198
A.Reference number: Z14198
A.Reference number: L191
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: L191
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A.Status: L191
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A/Accession: 263, 2830-2839, 1988
A/Accession: 263, 2830-2839, 1988
A/Accession: A29926
A/Accession: A
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A,Molecule type: DNA
A,Rosidues: 1-1664 <PUR>
A,Rosidues: 1-1664 <PUR>
C,Genetics: EMBL:X95720; NID:g1199839; PIDN:CAA65029.1; PID:g1199844
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A;Map position: 15R
C;Superfamily: Trypanosoma DNA-directed RNA polymerase I largest chain
C;Superfamily: Trypanosoma DNA-directed RNA polymerase I largest chain
C;Keywords: DNA binding; nucleotidyltransferase; transcription; zinc finger
F;62-78/Region: zinc finger CCHH motif
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submitted to the Protein Sequence Database, July 1996
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A;Introns: 66/3; 81/2; 170/2
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                                                    Reference number: S67246
Accession: S67250
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A;Reference number: 867392
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A,Molecule type: DNA
A,Residues: 1-191 <STG
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$70582
botulinum neurotoxin type Dsa precursor - Clostridium botulinum phage d-sA
C;Species: Clostridium botulinum phage d-sA
A;Note: host Clostridium botulinum type D (strain South Africa)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: $70582
B;Moriishi, K.; Koura, M.; Abe, N.; Fujii, N.; Fujinaga, Y.; Inoue, K.; Ogumad, K.
Biochim, Biophys. Acta 1307, 123-126, 1996
A;Title: Mosaic structures of neurotoxins produced from Clostridium botulinum types C an A;Reference number: $70582; MUID:96283801; PMID:8679691
A;Reference number: $70582
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;References: EMBL:D38442; NID:g1374775; PIDN:BAA07477.1; PID:g1374776
C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu a disulfide bond. The heavy chain mediates the binding of toxin to the presynaptic membr C;Superfamily: tetanus toxin
C;Keywords: disulfide bond; neurotoxin; transmembrane protein
C;Keywords: disulfide bond; neurotoxin type Dsa light chain #status predicted <MATI>F;448-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MATI>F;448-1285/Product:
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DNA-directed RNA polymerase (EC 2.7.7.6) I 190K chain - yeast (Saccharomyces cerevisiae)

NA-ternate names: DNA-directed RNA polymerase A 190K chain; protein O6276; protein YOR3

C;Species: Saccharomyces cerevisiae

C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004

C;Accession: S67250; A29926; S67396

R;Goffeau, A.; Purnelle, B.
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Matches 6; Conserv
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Matches 6; Conserv
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ઠે d RESULT 5

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very-late factor 1 protein - Orgyja pseudotsugata nuclear polyhedrosis virus
Very-late factor 1 protein - Orgyja pseudotsugata nuclear polyhedrosis virus, OpkNPV
C;Species: Orgyja pseudotsugata nuclear polyhedrosis virus, OpkNPV
C;Accession: T10349
R;Adrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
A;Title: The sequence of the Orgyja pseudotsugata multinucleocapsid nuclear polyhedros:
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10349
A;Accession: T10349
A;Accession: T10349
A;Accession: T10349
A;Accession: T10349
A;Residues: 1-374 <AHR>
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Mw, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-195 <STO>
A;Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:g10120423; PIDN:AAG13048.1; GSPDB:C
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted to the BMBL Data Library, September 1995
A, Description: An Arabidopsis thaliana cDNA encoding a lectin like protein. A, Reference number: S71252
A, Accession: S71252
A, Accession: S71252
A, Residues: 1-272 < HERA
A, Residues: 1-272 < HERA
A, Cross-references: UNIPROT: Q39205; EMBL: X91259; NID: G995618; PID: G995619
C; Superfamily: plant lectin
C; Keywords: lectin
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Accession: S71252
Rierve, C.; Lescure, B.
Submitted to the EMBL Data Library, September 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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17;
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Pred. No. 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
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62.5%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
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nes 5; Conservative
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18 FAVKFNFD 25
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                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: F14J22.14
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14075
R;de la Vega, H; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A;Reference number: 217872
A;Accession: T14075

                                                                                                                                                                                                                                                                                                                                                                                                     chitimase (EC 3.2.1.14) precursor - Bacillus circulans
C;Species: Bacillus circulans
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
C;Datesion: A38368
R;Matanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.
J. Biol. Chem. 265, 15659-15665, 1990
A;Pitle: Gene cloning of chitimase A1 from Bacillus circulans WL-12 revealed its evoluti
A;Reference number: A38368; MUD:90368776; PMID:2203782
A;Actession: A38368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F14J22.14 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Nar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (Spacession: H96532 Ascession: H96532 Ascession: H96532 Ascession: H96532 Ascession (Spacession: H96532 Ascession (Spacession: Ass.) Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-699 <WAT>
A;Cross-references: UNIPROT:P20533; GB:M57601; GB:J05599; NID:g1066341; PIDN:AAA81528.1;
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                   Length 191;
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Pred. No. 24;
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                                                                          DB 2;
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Pred. No. 58;
0; Mismatches
                                                                          Score 34; DB
Pred. No. 6.4;
0; Mismatches
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ilarity 75.0%;
Conservative C
                                                                          89.5%;
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                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                    167 FKKKYNFD 174
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
                                                                                                     Best Local Similarity Matches 6; Conserv
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RESULT 12

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A; Molecule type: DNA
A; Residues: 1-648 < SCH>
A; Cross-references: UNIPROT: P43634; EMBL: Z49975; NID: G886706; PIDN: CAA90276.1; PID: g8867
R; Benes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Ansorge, W.; Voss, H.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64920
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-648 cBEN>
A; Residues: 1-648 cBEN>
A; Cross-references: EMBL: 273270; NID: 91360478; PIDN: CAA97662.1; PID: e245801; PID: 9136047
A; Experimental source: strain S288C
R; Holmberg, S.; Schjerling, P.
R; Holmberg, S.; Schjerling, P.
A; Title: Cha4p of Saccharomyces cerevisiae activates transcription via serine/threonine
A; Reference number: S72236; MUID: 97044442; PMID: 8889513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cincers outer membrane protein homolog SefC - Salmonella enteritidis
CiSpecies: Salmonella enteritidis
Riclouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
Riclouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
A; Clouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
A; Clouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
A; Reference number: A40618; MUID:93239677; PMID:8097515
A; Reference number: A40618; MUID:93239677; PMID:8097515
A; Accession: C40618
A; Accession: C40618
A; Accession: C40618
A; Residues: DAA
A; Residues: 1-614 < CLO>
A; Cross-references: UNIPROT:P33388; GB:L11010; NID:G310649; PIDN:AAA27221.1; PID:G310650
C; Superfamily: outer membrane usher protein fimD
C; Superfamily: outer membrane usher protein fimD
C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Description: activation of CHA1; binds to UAS1(CHA) and UAS2(CHA) elements in CHA1 prof C.Superfemanly: GAH4 zinc binuclear cluster homology C;Reywords: DNA binding; nucleus C;Reywords: DNA binding; nucleus P;39-75/Domain: GAL4 zinc binuclear cluster homology <GAL4>
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A;Molecule type: DNA
A;Residues: 1-648 <br/>
A;Cross-treferences: EMBL:Z49975; NID:g886706; PIDN:CAA90276.1; PID:g886707
C;Genetics:
A;Gene: SGD:CHA4
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62.5%; Pred. No. 1.2e+02;
iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: SGD:S0004088; MIPS:YLR098c A;Map position: 12R C;Function:
                                  submitted to the EMBL Data Library, June 1995
A;Reference number: S59723
A;Accession: S59723
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62.5%;
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Best Local Similarity 62.5%
Best Local Si Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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620 FALEYNFD 627
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          R;Schjerling, P.
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Cipacies: Arabidopsis thaliana (mouse-ear cress)
Cipace: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
CiAccession: T08866
Riwaterston R.
Submitted to the EMBL Data Library, October 1997
A;Reference number: 216500
A;Accession: T08866
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-480 (MAT>
A;Residues: 1-480 (MAT>
A;Experimental source: cultivar Columbia
C;Generics:
C;Generics:
A;Gene: ATGS:A TW017A05.12
A;Map position: 4
C;Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology
F;7-470/Domain: acetate-COA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dispecies: Arabidopsis thaliana (mouse-ear cress)

C;Species: O2-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84554

R;Lin, X: Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R;Lin, X: Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R;Lin, X: Moffat, W.C.; White, O.; Bisen, J.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.;

Nature 402, 761-768, 1999

Nature 402, 761-768, 1999

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Recession: G84554

A;Scatus: preliminary

A;Rocession: G84564

A;Scatus: preliminary

A;Rocession: G84567

A;Rocession: C64567

A;Residues: 1-603 csro

A;Cross-references: UNIPROT:Q9SEY5; GB:AB002093; NID:g6598797; PIDN:AAF18674.1; GSPDB:GN

C;Genetics:
A;Gene: Ac2g17650

A;Map position: 2

C;Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology
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                                                                                                                                                                                                                hypothetical protein A_TM017A05.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS9723
transcription activator CHA4 - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein L255; protein YLR098c
C;Species: Saccharomyces cerevisiae
C;Species: Acadaromyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: SS9723; S64932; $72236
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Pred. No. 89;
1; Mismatches 2; Indels
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70;
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O1710 chenchana t
Q8Guaz nicotiana t
Q8Guyz clostridium
Q9107 candida gla
Q6cix4 kluyveromyc
O17414 anopheles g
Q93yf6 nicotiana s
Q91ry0 arabidopsis
O8109 arabidopsis
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                                          October 26, 2004, 15:27:03; Search time 44.6154 Seconds (without alignments) 103.171 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q97LU5
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2: uniprot_trembl:*
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ALIGNMENTS

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Gaps
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10-MAY-2004 (TREMBLEEL. 27, Last sequence update)
10-MAY-2004 (TREMBLEEL. 27, Last sequence update)
Hyporhetical protein P0486503.18.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza sativa.
                                                                                                                                                        Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, I
clone:P0486G03.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 262,
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005002; BAD17213.1; -.
InterPro; IPR003175; CDI.
Pfam; PF02234; CDI.
Hypothetical protein.
SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;
                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein P0486G03.18.
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Pred. No. 24;
0; Mismatches
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262 AA
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Best Local Similarity 75.0%;
Matches 6; Conservative
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PRELIMINARY;
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171 FSEKYNFD 178
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SEQUENCE 196
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=30069,
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MEDLINE=99329903; PubMed=10409053;
Fountain M.D., Renz A., Beck E.;
"Isolation of a cDNA encoding a G1-cyclin-dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sprmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Chenopodium.
NCBI_TaxID=3560;
                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93324849; PubMed=9662472;

A de la Vega H., Specht C.A., Liu Y., Robbins P.W.;

de la Vega H., Specht C.A., Liu Y., Robbins P.W.;

de la Vega H., Specht C.A., Liu Y., Robbins P.W.;

T "Chitinases are a multi-gene family in Aedes, Anopheles and Drosophila.";

Insect Mol. Biol. 7:233-239(1998).

R EMBL, AF026499; AA881857.1; -.

R HSSP; Q13231; 1LG2.

R HSSP; Q13231; 1LG2.

R GO; GO:0016787; F:Metabolism; IEA.

GO; GO:0016787; F:Metabolism; IEA.

R TheerPro; IPRO1223; Glyco.hydro_18.

R InterPro; IPRO1253; Glyco.hydro_18.

R FRONITE; PS01095; CHITINASE_18; PARTIAL.
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                                                                                     Score 36; DB 2; Length 262;
Pred. No. 24;
0; Mismatches 2; Indels
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Pred. No. 16;
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EMBL, AP005002; BAD17213.1; -.
Hypothetical protein.
SEQUENCE 262 AA; 27138 MW; 42ECB5C8276C0726 CRC64;
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113 AA; 13188 MW; 5EA7DCA6B54B4B97 CRC64;
                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Chitinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyclin-dependent kinase inhibitor protein.
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                                                                                     94.78;
75.0%;
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75.08;
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01-JUN-1998 (TrEMBLrel. 06,
                                                                            Query Match
Best Local Similarity 75.0
Matches 6, Conservative
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Best Local Similarity
Matches 6; Conserv
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BMBL, AM517189; CAD56808.1, -

CO, GO:0005634; Cruclede. 1 BA.

GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . ., IEA.

GO; GO:0016501; F:kinase activity; IEA.

GO; GO:0007050; F:kinase activity; IEA.

InterPro, IPR003175; CDI.

Pfam; PF02234; CDI.

SEQUENCE 207 AA; 23278 WW; F5AE70AD2261BC2D CRC64;
from suspension-cultured photoautotrophic chenopodium rubrum cells."; Plant Physiol. 120:339-339(1999). EMBL; AJ002113; CA805215.1; -. PIR; T09968; T09968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Jasinski S., Saraiva Leite C., Domenichini S., Stevens R., Raynaud (
Perennes C., Bergounioux C., Glab N.;
"NKKIS2, a novel tobacco cyclin-dependent kinase inhibitor
differentially expressed during the cell cycle and plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterlamids, Solanales, Solanaceae, Nicotiana.
                                                                                                           GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0007050; P:cell cycle arrest; IEA.
InterPro; IPR003175; CDI.
Pfam; PF02234; CDI; 1.
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Pred. No. 30; 2; Indels
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                    196 AA; 21685 MW; 150349F7ED82A6B2 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
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OrderedLocusNames=MYPE7310;
Mycoplasma penetrans.
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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BXD_CLOBO
P19321;
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NR GO; GO: 0000166; F: nucleotide binding; IEA.

GO; GO: 0000166; F: nucleotide binding; IEA.

GO; GO: 0000166; F: nucleotide binding; IEA.

GO; GO: 0000160; F: transcription factor activity; IEA.

GO; GO: 0000160; F: transcription factor activity; IEA.

DR InterPro; IPR003593; AAA ATPase.

NR InterPro; IPR0030957; HTH Pis.

NR InterPro; IPR0000197; HTH Pis.

DR InterPro; IPR0000197; HTH Pis.

DR InterPro; IPR0000197; HTH Pis.

DR InterPro; IPR0000197; PPR.

NR InterPro; IPR0000197; PPR.

NR InterPro; IPR0000197; PPR.

NR InterPro; IPR000918; Sig54_interact.

DR Pfam; PF00586; PPR.

NR Pfam; PF00586; PPR.

NR Pfam; PF00586; PPR.

NR Pfam; PF00586; PPR.

NR Pfam; PF00587; AAA; 1.

DR Pfam; PF00189; AAA; 1.

DR TIGRPAMS; TIGR01199; HTH fis; 1.

TIGRPAMS; TIGR01199; HTH fis; 1.

TIGRPAMS; TIGR00199; HTH fis; 1.
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                                                                                                                                                                                                Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5233-5300(2002).
EMBL. APOGATA; BAC44525.1;
Complete porteome, Hypothetical protein.
SEQUENCE 442 AA; 50767 MW; 240200E4470ED768 CRC64;
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21559325. PubMed=11466266;

DOI=10.1128/JBs.183.16.4823-4838.2001;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucete-Stamm L.A., Soucaille P., Daly W.J., Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium clostridium acetobutylicum.";

"Bacteriol. 183:4823-4838(2001).

"SIMILARITY: Contains I sigma-54 factor interaction ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium acetobutylicum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Bacteria; Firmicutes, Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=28227;
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PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                              MEDLINE=22354719; PubMed=12466555;
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EMBL; AE007560; AAK78439.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 FISKYNFD 67
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                                                                                                       SEQUENCE FROM N.A.
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NCBI_TaxID=1488;
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RC STRAIN=89017546; PubMed=802560;

RX MEDLINE=99017546; PubMed=802560;

RA Nakajima H., Inoue K., Ikeda T., Fujinaga Y., Sunagawa H., Takeshi K., Oyama T., Watanabe T., Inoue K., Oguma K.;

RA Nakajima H., Inoue K., Ikeda T., Fujinaga Y., Sunagawa H., Takeshi K., Oyama T., Watanabe T., Inoue K., Oguma K.,

RA Nakajima H., Inoue K., Ikeda T., Oyama K.,

RT Molecular composition of the 165 toxin produced by a Clostridium type D strain, 1873.",

RI Microblol. Immunol. 42:599-605(1998).

RE ENGLIA: Abarisalar Sandase activity; IEA.

RG, GO.0003405; P:pethogenesis, IEA.

RG, GO.000405; P:pethogenesis, IEA.

RG, GO.0006608; P:profectolysis and peptidolysis; IEA.

RG, GO.0006608; P:profectolysis and peptidolysis; IEA.

RINEPRO; IPR006985; ConAlinum.

RINEPRO; IPR006985; ConAlinum.

RINEPRO; IPR006985; ConAlinum.

RINEPRO; IPR006025; Pept M.Zn.

REMINTS; PR00760; BONTOXILYSIN.

REMINTS; PR00760; BONTOXILYSIN.

RTCDM; PR001142; PR01140; ANT.

RTCDM; PR001153; ANT.

RTCDM; PR001151; AA; 146742 MW; 3CSOF46CB233E2D6 CRC64;
PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS0045; SIGMA54_INTERACT_4; 1.
ATP-binding; Complete professore; DNA-binding; Transcription regulation.
SEQUENCE 627 Ap.; 71082 WW; 4A652FA3AB362AD0 CRC64;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-S-014-1004 (Rel. 44, Last annotation update)
Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BONI/D)
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                                                                                                                            92.1%; Score 35; DB 2; Length 627; 75.0%; Pred. No. 94; 2; Indels tive 0; Mismatches 2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 75.v.
                                                                                                                                                     Best Local Similarity 75.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                       311 FVAKYNFD 318
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Name=botD;
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Neurotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  SEQUENCE FROW N.A.
STRAIN=Type D / CB-16;
STRAIN=Type D / CB-16;
Sunagawa H., Obyama T., Watanabe T., Inoue K.;
Sunagawa H., Obyama T., Watanabe T., Inoue K.;
The complete amino and sequence of the Clostridium botulinum type D neurotoxin, deduced by nucleotide sequence analysis of the encoding phage d-16 phi genome.";
J. Vet. Med. Sci. 54:905-913 (1992).
                                                                                                                                                                                                                                                                                                                                                              STRAIN=TYDE D / South African, and Type D / D-1873;
MEDLINE=89339741; PubMed=2668193;
Moriishi K., Syuto B., Kubo S., Oguma K.;
"Molecular diversity of neurotoxins from Clostridium botulinum type D
                               SEQUENCE FROM N.A.
STRAIN=Type D / BVD/3;
MEDLINE=91016883; PubMed=2216736;
Binz T., Kurazono H., Popoff M.R., Eklund M.W., Sakaguchi G.,
Kozaki S., Krieglstein K., Henschen A., Gill D.M., Niemann H.;
Nucleotide sequence of the gene encoding Clostridium botulinum
                                                                                                                                    neurotoxin type D.";
Nucleic Acids Res. 18:5556-5556(1990)
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InterPro; IPR011065; Kunitz like.
InterPro; IPR000395; Peptidase_M27.
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EMBL; S49407; AAB24244.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S11455; S11455.
HSSP; P10844; 1F31.
                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE.
 NCBI_TaxID=1491;
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"Mosaic structures of neurotoxins produced from Clostridium botulinum types C and D organisms.";
Biochim. Biophys. Acta 1307:123-126(1996).
BMBL; D38445; BAA07477.1; -.
MHSSP; P10844; 1F31.
MEROPS; M27.002; -.
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InterPro; IPR006025; Pept M Zn_BS.
PRAM; PR01742; Peptidase M27; 1.
PRINTS; PR00760; BONYOXILYSIN;
ProDom; PD001963; Bontoxilysin; 1.
ProSOITE; PS00142; ZNC PROTEASE; 1.
Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin;
Transmembrane; Zinc.
                                                                                                                                                                                                                                                                                                                    Botulinum neurotoxin D light-chain.
Botulinum neurotoxin D heavy-chain.
Zinc (catalytic) (By similarity).
By similarity.
Zinc (catalytic) (By similarity).
Interohain (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-South African, MEDLURE-96283801; MEDLURE-96283801; PubMed-8679631; Moriishi K., Koura M., Abe N., Fujii N., Fujinaga Y., Inoue K., Ogumad K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1; Length 1276; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ND -> PV (in strain D-SA).

ND -> LQ (in strain D-1873).

R -> Q (in strain D-SA).

R -> T (in strain D-SA).

R -> F (in strain D-1873).

A -> D (in strain D-1873).

K -> N (in strain CB16).

N -> K (in strain CB16).

Q -> R (in strain CB16).

Q -> R (in strain CB16).

MW; C18C50F46C8233BZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147365 MW; EEDE98E4ECA6C413 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008233; P:peptidase activity, IEA.
GO; GO:0009405; P:pethogenesis; IEB.
GO; GO:0009405; P:pethogenesis; IEB.
InterPro; IPR01159; Botulinum.
InterPro; IPR01159; Botulinum.
InterPro; IPR01059; Kunitz like lec_gl.
InterPro; IPR001395; Peptidase_M27.
InterPro; IPR001395; Peptidase_M27.
InterPro; IPR001395; Peptidase_M27.
InterPro; IPR001305; Peptidase_M27.
INTERPRO; IPR001305; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom, PD001963, Botulinum, 1.
PROSITE, PS00142, ZINC_PROTEASE, UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 Q -
146871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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18
452
457
457
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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01-MAR-2004
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Length 1285;

92.1%; Score 35; DB 2;

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SEQUENCE FROM N.A.
STRAIR=ATCC 10895;
PubMed=15001715,
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
Gaffney T.D., Philippsen P.;
"The Ashbya gossypii genome as a tool for mapping the ancient
Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINE-ATCC 10895;
Voegalia-ATCC 10895;
Voegalia-ATCC 10895;
Philippsen P.;
Philippsen P.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AR016893; AR522294.1;
SEQUENCE 1640 AA; 182887 MW; 4B89F52FC18BCDF0 CRC64;
                                                                                                                 SEQUENCE FROM N.A.
STRAINE-ATCC 10895;
Voegoli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T., Philippsen P.;
Philippsen P.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AE016893; AAS52294.1;
AGD; ADR374C;
Luedi P., Choi S., Wing R.A., Flavier A.
Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A. Gaffney T.D., Philippsen P.;
"The Ashbya gossypli genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
92.1%; Score 35; DB 2; Length 1640;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                               R InterPro; IPR000345; Cytc heme BS.
R InterPro; IPR000559; RNA_DolA_N.
R InterPro; IPR000725; RNA_DolA_N.
R InterPro; IPR007080; RNA_DolA_N.
R InterPro; IPR007080; RNA_DolA_DolA_DolA_N.
R InterPro; IPR007080; RNA_DolRpbl_3.
R InterPro; IPR007081; RNA_DolRpbl_4.
R InterPro; IPR007081; RNA_DolRpbl_5.
R Pfam; PF004987; RNA_DolRpbl_1; 1.
R Pfam; PF004983; RNA_DolRpbl_2; 1.
R Pfam; PF004983; RNA_DolRpbl_2; 1.
R Pfam; PF00498; RNA_DolRpbl_4; 1.
R Pfam; PF00498; RNA_DolRpbl_4; 1.
R SWART; SW00663; RNA_DolRpbl_4; 1.
R SWART; SW00663; RNA_DolRpbl_5; 1.
R SWART; SW00163; RNA_DolRpbl_6; 1.
R SWART; SW00184; CYTOCHROME C; UNKNOWN 1.
R PROSTIE; PR01A A4; 182887 MW; 4B89F52FC18BCDF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.1%; Score 35; DB 2; Length 1640; 75.0%; Pred. No. 2.5e+02; ive 0; Mismatches 2; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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STRANT=ATC: 10895;
PubMed=1501715;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAINED-4947;

X MEDLINE=2165974; PubMed=11713244;

MEDLINE=2165974; PubMed=11713244;

MEDLINE=2165974; PubMed=11713244;

MEDLINE=2165974; PubMed=11713244;

In vitro reconstitution of the Clostridium botulinum type D

In Torogenitor toxin."; J2550-2656(2002).

In Band, AB037920; Band, AB0395; Peptidase M27, InterPro; IPR0000395; Peptidase M27, InterPro; PR00142; PR00142; ZINC_PR0TBASE; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashbya gossypii (Yeast) (Eremothecium gossypii).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1285 AA; 147351 MW; B63AFA487D570680 CRC64;
                         2; Indels
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Q759A3;
G5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last senotation update)
                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
        Pred. No. 2e+02;
; Mismatches
                                                                                                                                                                                                       PRT; 1285 AA
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0
        75.0%;
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        Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Clostridium botulinum.
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                                                                                                FSEKYNFD 333
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                                                                   1 FXXKYNFD 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1491;
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Name=ADR374C;
                                                                                                                                                                                                                                                                                                     Neurotoxin.
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                                                                                                      326
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Q9LBR1
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Search completed: October 26, 2004, 15:39:25
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TrEMBirel. 28, Last sequence update)
(TrEMBirel. 28, Last annotation update)
Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleysagen C., Despons L., Boyer J., Cattolico L., Confanioleri F., de Daruva A., Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Leau I., Muller H., Nicald J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Sileau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A., Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
51-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
06-FNAmes=CAGLOE055009;
Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00190; CYTÖCHROME C; UNKNOWN 1.
1643 AA; 184865 WW; FD2B3ED14021FC18 CRC64;
                                                                                                                                                                                                                                                                             PRT; 1643 AA
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InterPro; IPRO07086; RNA_DOI Rpbl_1.
InterPro; IPRO07086; RNA_DOI Rpbl_3.
InterPro; IPRO07081; RNA_DOI Rpbl_4.
InterPro; IPRO07081; RNA_DOI Rpbl_5.
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Rpb1_3; 1.
Rpb1_4; 1.
Rpb1_5; 1.
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InterPro; IPR000345; CytC_heme_
InterPro; IPR006592; RNA_polA_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in yeasts.";
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75.0%;
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Wincker P., Souciet J.L.;
"Genome evolution in yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04997; RNA_pol_RpPfam; PF04623; RNA_pol_RpPfam; PF04993; RNA_pol_RpPfam; PF04998; RNA_pol_RpPfam; PF04998; RNA_pol_RpRART; SMO663; RPOLA_N; PROSITE; PS00190; CYTÖCHF
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                            1432 FISKÝNFD 1439
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                          1 PXXKYNFD
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01-0CT-2004 (01-0CT-2004 (01-0CT-2004)
Strain NRRL Y
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106 FV16
10 FV16
10 FV16
10 FV1
10
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Agle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Rabre E., Falrhead C., Ferry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Low P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lewur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Streub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Weethof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
T. "Genome evolution in yeasts.";
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                                                                         Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
NCBI_TaxID=28985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR82126; CAG98823.1, -
SEQUENCE 1653 AA; 185832 MW; E1A9732COAAE8387 CRC64;
ORFNames=KLLA0F23243g;
Kluyveromyces lactis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 430:35-44(2004)
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STRAIN=NRRL Y-1140;
GENOLEVURES;
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STRAIN=NRRL Y-1140;
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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to soreen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to ICK protein, forms which have decreased or absorrant activity compared ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
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AAX08847
AAR844650
AAR8465029
AAX08842
AAX08843
AAX08843
AAX08843
AAX08843
AAX08815
AAX08815
AAX08813
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AAY08844
AAY08816
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13-OCT-2000; 2000US-0241219P.
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(CROP-) CROPDESIGN NV
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   \begin{smallmatrix} \mathsf{D} & \mathsf{D} 
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07880010848987886010848
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                                                                                                                                                                                                                                           October 26, 2004, 15:19:44 ; Search time 44.6154 Seconds (without alignments) 64.324 Million cell updates/sec
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Aaw98180
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                                         5.1.6
Compugen Ltd.
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                                         version 5
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Maximum Match 100%
Listing first 45 summaries
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AAE25107
AAW98180
AAE25111
AAG5721
ABG65712
ABG65712
AABG65671
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AAY08818
AAG42859
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AAY08812
AAY08817
AAY44335
AAG15426
AAG42858
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length: 2000000000
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ABG65677 RESULT

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Modifying plant cell development using nucleic acid encoding inhibitor of cyclin-dependent kinase, or correspnding antisense sequence, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present protein sequence is ICN7, which inhibits A. thaliana Cyclin-Dependent Kinase (CDK). Interactor of Cyclin 7 (ICN7) interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional and sequence similarity with ICK1. Growth, morphogenesis, multiplication, enlargement, differentiation and maturation of plant cells can be modified by transforming them with nucleic acid encoding CDK inhibitor or antisense construct complementary to the inhibitor gene, operably linked to a tissue-specific promoter. The transgenic plants exhibit alteration of traits such as petals, male sterility and ability to set seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2; ICN2; ICN5; ICN7; ICN8; ICDK; morphogenesis; maturation; enlargement; plant breeding; growth.
                                                                                                                                                                                             Cyclin-Dependent Kinase inhibitor; CDK; Interactor of Cyclin 7; ICN7; Cdc2a, D-class cyclin; CycD1; CycD2; CycD3; morphogenesis; antisense construct; tissue-specific promoter; transgenic plant; male sterility.
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Pred. No. 11;
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(UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
(CANA ) NAT RES COUNCIL CANADA.
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                                                                                                                                          Arabidopsis thaliana CDK inhibitor, ICN7.
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                                                                                     29-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to the DNA and protein sequences of novel isolated the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for maturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of the protein, forms which made decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
                                                                                                                 Gaps
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                         Score 38; DB 5; Lengtn 0,
Pred. No. 1.7e+06;
....hes 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant; inhibitor of cyclin dependent kinase; ICK.
                                                                                                                 0; Mismatches
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ID AAY44339 standard, protein, 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                   ABG65677 standard; protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001; 2001WO-IB001492.
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13-OCT-2000; 2000US-0241219P.
                                                        95.0%;
85.7%;
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                                                     Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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LSGRYEW 8
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Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG65677;
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Gaps

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RESULT 3

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us-09-574-735c-35.rag

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The present sequence is F166, a new cyclin-dependent kinase (CDK)

inhibitor of Arabidopsis thaliana encoded by a CDNA clone (see AAX25016)

cobtained by two-hybrid screening using CDC2aA4 procein as batt. Recults

established that several CDK inhibitors (see also AAW98179) and AAW98181)

cxist in plants and that these inhibitors are expressed at different time

compaints and may have different functions during the development of the

plant. CDK inhibitors, nucleic acids, antibodies, promoter sequences,

related recombinant DNA and vectors are all useful: for diagnosis (no

compaints of the compaint of CDK, for modulating growth inhibition in

plants caused by environmental stress, for inducing male or female

sterility; for altering cell division progression in plants, bacteria,

fungi, insect and animal cells; and to screen for agonists or natagonists

that are potentially useful as growth regize or resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant development, cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2; ICN2; ICN7; ICN7; ICN8; ICDK; morphogenesis; maturation; enlargement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                               Landrieu I;
                                                                                                                                                                                                            DNA encoding inhibitor of cyclin-dependent kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38;
Pred. No.
                                                                                                               De Almeida J,
                                                                                                                                                                                                                                                Claim 1a; Page 76-77; 88pp; English.
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                    97EP-00202838
97EP-00204111
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Best Local Similarity 85.,
6, Conservative
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plant breeding; growth.
                                                                                                               De Veylder L,
                                                                        (CROP-) CROPDESIGN NV.
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N-PSDB; AAX25016.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 216 AA;
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                    16-SEP-1997;
24-DEC-1997;
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                                                                                                               Inze D,
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AAE2511
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    .216
    /note= "this protein region is specifically claimed in
Claim 1(c)"

                                                                                                                                                                                                                                                                                                                                          Modifying plant development, e.g. growth or maturation, which is particularly useful in plant breeding, by introducing nucleic acids coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins that bind to CDK inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL66; plant development; transgenic plant; cell cycle; growth regulator;
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                                                                                                                                                                                    (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
(UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 10A; 89pp; English.
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                                                                                                             18-DEC-2001; 2001WO-CA001825.
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                                                                                                                                                                                                                                                Zhou Y, Fowke LC;
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 137 AA;
                                    WO200250292-A2
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                                                                                                                                                                                                                                                Wang H,
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Best Loc Matches

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RESULT 5 AAW98180

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This invention relates to a novel method for altering one or more plant corracteristics. Specifically, it refers to identifying genes that are up or down regulated in transgenic plants overexpressing the heterodianeric E2Pa/DPa transcription factor of Arabidopsis and using these sequences to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , g
                                                                                                                                                     The invention relates to a method for the development of a plant. The method involves introducing into a plant cell a nucleic acid encoding a protein that binds or interacts with a cyclin-dependent kinase (CDK) inhibitor polypeptide (such as ICRI, ICK2, ICN2, ICN6, ICN7, ICN8 and ICDK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the degradation of a CDK inhibitor polypeptide. The method is useful for modifying the growth and development of plants e.g. morphogenesis, growth, multiplication, enlargement, differentiation or maturation of a cell or plant. It is particularly useful in plant breeding. The present sequence is A. thaliana ICN7 full-length protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                              Modifying plant development, e.g. growth or maturation, which is particularly useful in plant breeding, by introducing nucleic acids coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant, transgenic, E2Fa/DFa transcription factor; growth regulator; animal feed product; thale cress, cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                            95.0%; Score 38; DB 5; Length 222; 85.7%; Pred. No. 18; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 246; 134pp; English.
                                                                                                                          Disclosure; Fig 10B; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN72351 standard; protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vlieghe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2003; 2003WO-EP011658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L8-OCT-2002; 2002EP-00079408
                                                                    coding for cyclin-aependent that bind to CDK inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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Best Local Similarity
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N-PSDB; AAD40771
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                                                                                                                                                                                                                                                                                                                                                             Sequence 222 AA;
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Matches
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atter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, c anzymes, therapetuics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endorseduplication, blochmistry, signal cransduction, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers curing transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall biosythesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.
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8
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Pred. No. 18;
0; Mismatches
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13-OCT-2000; 2000US-0241219P.
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85.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
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This invention relates to the DNA and protein sequences of novel isolated trex (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Droual A, Mironov V,
                                                                                                                                                                                      Plant; inhibitor of cyclin dependent kinase; ICK.
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85.7%; Pred. No. 2.6;
cive 0; Mismatches
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Hatzfeld Y;
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2000US-0241219P
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N-PSDB; ABK93951.
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Matches 6, Conserv
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                                                                                                                                                                                                                           Oryza sativa.
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13-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to the DNA and protein sequences of novel isolated the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
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                                                                                         Score 37; DB 5; Length 8;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; inhibitor of cyclin dependent kinase; ICK.
                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               Plant ICK protein conserved motif 1 #20.
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                                                                                                                                                                                                                                                                                                 ABG65712 standard; peptide; 8 AA.
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13-OCT-2000; 2000US-0241219P.
                                                                                           92.5%;
85.7%;
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                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                       Sequence 8 AA;
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Frankard ' Hatzfeld '

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ABG65712;

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à g ABG65712

Inze D;

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Gaps

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5; Length 22; Indels

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The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequence is the soybean CDKI clone $12.pk0008.d2 as described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean; plant growth inhibitor.
          Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0008.d2:fis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 3; Length 38;
Pred. No. 4.5;
0; Mismatches 1; Indels
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                                                                        42; 58pp; English.
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Best Local Similarity 85.,
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38 AA;
                                                                            Page
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                                                                          Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP01951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the soybean cyclin-dependent kinase indicated (CDKI). Its coding sequence was isolated by searching a soybean seedling CDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI si involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean; plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0008.d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                     Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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Pred. No. 4.5;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 42; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP01942 standard; protein; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cahoon RE;
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                                                                                                                                                           99US-0128192F
                                                                                                                    06-APR-2000; 2000WO-US009106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7
Matches 6; Conservative
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N-PSDB; AAA95278.
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N-PSDB; AAN02392.
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                                                                                                                                                                                                                                         Weng Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200060087-A2
                                    WO200060087-A2
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                                                                                                                                                           07-APR-1999;
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Glycine max
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                                                                                                                                                                                                                                         Klein TM,
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AAY08846 standard; protein; 138

RESULT 15

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The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the soybean CDKI clone $12.pk0008.d2:fis as described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean, cyclin-dependent kinase inhibitor; cell cycle; cell division; CDKI; cell growth, herbicide.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclin dependent kinase inhibitor sequences, useful for identifying
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                                                                                                                                     Length 87;
                                                                                                                                     Score 37; DB 3;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                              Soybean cyclin-dependent kinase inhibitor #2.
                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             herbicides and plant growth inhibitors.
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                                                                                                                                                                                                                                                                                                      AAB27253 standard; protein; 87
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                                                                                                                                    92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000WO-US009106.
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85.7%;
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N-PSDB; AAA95287.
                                                                                                                                                                                                                          76 LEGRYEW 82
                                                                                                                                                Local Similarity
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                                                                                                          Sequence 87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060087-A2.
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                                                                                                                                                                                                                                                                                                                                    AAB27253;
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Matches
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This invention describes (1) a protein that inhibits p27 and thereby arrests p27-induced inhibition of cell proliferation, (2) the protein of (1) comprising at least part of the amino acid sequence of murine p163.

(3) a protein that can be derived from the protein of (2) by deletion of (3) a protein that can be derived from the protein of (2) by deletion of all amino acid compressing at the protein of (2) by deletion of all amino acid sequences other than the p27 binding domain, (5) a protein that is the unan or other ammalian species homologue of a protein that is the unan or other ammalian species homologue of a protein that is the unan or other ammalian species homologue of a protein as above, (9) antisense mucleic acids complementary to portions of the DNA encoding the p163 protein, (7) antibodies and antibody fragments that bind to the Ran binding domain of a protein as above, (9) antisense mucleic acids complementary to portions of the Coding for an antisense mucleic acids complementary to portions of the proliferation of a cell, in which DNA coding for the antisense mucleic acid as in (9) for inhibiting the proliferation of a cell, in which DNA coding for the antisense mucleic acid as in (9) for inhibiting the coding for an antisense uncleic acid as in (8) for inhibiting the protein as above in a cell. The DNA of (6) can be used for detection of a cell, in which DNA coding for the antisense and is introduced into the target cell as naked acid onstruct containing the DNA of (6) inhead to a cell. The DNA of (6) can be used for detection of a cell as above in a cell. The DNA of (6) can be used for detection of a protein a above in a cell. The DNA of (6) can be used for detection of a corresponding protein in cells, the substance that permits expensed to between the proteins and their cellular binding partners of p163 or substance that inhibition of the interaction between the proteins and their cellular binding of a labelled binding partner of p163 (especially p27 or Ran) is placed by a protein and passed 
                                                                                                                                            p163, murine, p27 inhibitor; p27-induced inhibition; cell proliferation; p27 binding domain; Ran binding domain; detection; screening; malignancy; tumour; mutant; p27 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New p27-inhibiting protein p163 and DNA - useful for detection and/or quantification of p163 mRNA.
                                                                                                               Murine mutant p27 protein from clone #850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (HMRI ) HOECHST MARION ROUSSEL DEUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sedlacek H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 28; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                   98EP-00123708.
                                                                                                                                                                                                                                                                                                                                                                                                          97DE-01056975.
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buergin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-349237/30.
                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-1997;
                                                                          13-AUG-1999
                                                                                                                                                                                                                                                                                                                           30-JUN-1999.
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Conservative

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Best Loca Matches

Local Similarity

LEGRYEW 82

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2 LXGRYEW 8

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SQ Sequence 138 AA;

Query Match 92.5%; Score 37; DB 2; Length 138; Best Local Similarity 85.7%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 1; Indels

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2 LXGRYEW 8 | | | | | | | 55 LEGRYEW 61

ò QC Search completed: October 26, 2004, 15:36:52 Job time: 45.6154 secs

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Sequence

Sequence 1, Sequence 3, Sequence 4, Sequence 6, Sequence 6,

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Sequence 2, 3 Sequence 26, 5 Sequence 26, Seguence 2, 1 Seguence 22,

OM protein

Run on:

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Sequence 56, Application US/09215221
Facent No. 626562
Fatent No. 626634
Fatent Patent No. 626637
Fatent No
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Patent No. 6710227

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: De Veylder, Lieven

APPLICANT: De Veylder, Lieven

APPLICANT: De Veylder, Lieven

APPLICANT: Landrieu, Isabelle

TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

FILE REFERENCE: 1187-2

CURRENT APPLICATION NUMBER: US/09/526,597D

CURRENT PILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 222;
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US-08-794-002-6
US-08-854-0398-6
US-08-275-9838-1
US-08-275-9838-1
US-08-275-9838-3
US-08-406-588-3
US-08-406-588-3
US-08-406-6
US-08-794-002-2
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US-08-794-002-2
US-09-854-0398-2
US-09-854-038-2
US-09-854-038-2
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Pred. No. 6.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%;
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Best Local Similarity 85.,
                             LSGRYEW 217
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   TYPE: PRT
ORGANISM: Murine
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US-09-215-221-56
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LENGTH: 135
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Sequence 56, Appl
Sequence 55, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 52, Appl
Sequence 6, Appli
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                                                                                                                                                                                                               October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds (without alignments) 40.099 Million cell updates/sec
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Sequence 18,
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Sequence 18,
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Sequence 1
Sequence 1
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- 2004 Compugen Ltd.
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US-09-215-221-56
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US-09-215-221-57
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           using sw model
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Gapop 10.0 , Gapext 0.5
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US-09-215-221-51
Sequence 51, Application US/09215221
; Patent No. 6265562
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US-09-215-221-53
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US-09-215-221-51
             85.7%;
        Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6, Conservative
                                                                                                            55 LEGRYEW 61
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                                                                        2 LXGRYEW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Murine sp.
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ORGANISM: Murine sp.
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| Patent No. 6265562 |
| Patent No. 6265562 |
| General INFORMATION: |
| APPLICANT: BILERS, MARTIN |
| APPLICANT: BILERS, MARTIN |
| APPLICANT: BURGIN, ANDREA |
| APPLICANT: BURGIN, ANDREA |
| APPLICANT: SEDACK, HANS-HARALD |
| TITLE OF INVENTION: NUMBER OF CYCLIN-DEPENDANT KINASES AND USES THEREOF |
| TITLE OF INVENTION NUMBER: 197 80 975.7 |
| CURRENT FILING DATE: 1998-12-18 |
| PRIOR APPLICATION NUMBER: 197 56 975.7 |
| PRIOR APPLICATION NUMBER: 197 56 975.7 |
| SEQ ID NOS: 57 |
| SEQ ID NO 55 |
| LENGTH: 180
                                                                                                                                                                                                                                                                           RESULT 3
US-09-215-221-50
| US-09-215-221-50
| Sequence 50, Application US/09215221
| Patent No. 6265502
| GENERAL INFORMATION:
| APPLICANT: BILERS, MARTIN
| APPLICANT: BUERGIN, ANDREA
| APPLICANT: BUERGIN, ANDREA
| APPLICANT: BUERGIN, MANS-HARALD
| TITLE OF INVENTION: INHIBITIORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
| FILE REPERENCE: 026083/0192
| CURRENT APPLICATION NUMBER: 197 56 975.7
| PRIOR PILING DATE: 1998-12-18
| PRIOR FILING DATE: 1997-12-20
| NUMBER OF SEQ ID NOS: 57
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 50
| LENTH: 180
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                                                                                            92.5%; Score 37; DB 3; Length 135;
85.7%; Pred. No. 5.8;
ive 0; Mismatches 1; Indels
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85.7%; Pred. No. 7.7;
1ive 0; Mismatches 1; Indels
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                              r OTHER INFORMATION: mutated p27 US-09-215-221-56
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US-09-215-221-50
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                          Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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55 LEGRYEW 61
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ORGANISM: Murine sp.
                                                                                                                                                                              2 LXGRYEW 8
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| FERENT NO. 0.4620504
| GENERAL INFORMATION MARTIN
| APPLICANT: BILERS, MARTIN
| APPLICANT: BUERGIN, ANDREA
| APPLICANT: BUERGIN, ANDREA
| APPLICANT: SELDACEK, HANS-HARALD
| TITLE OF INVENTION: UNCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
| TITLE OF INVENTION: UNLEST ACID OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
| FILE REPERENCE: 026083/0192
| CURRENT APPLICATION NUMBER: 197 S6 975.7
| FRIOR APPLICATION NUMBER: 197 S6 975.7
| FRIOR PELING DATE: 1997-12-20
| NUMBER OF SEQ ID NOS: 57
| SEQ ID NO 5: 57
| SEQ ID NO 5: 194
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19-09-215-221-53
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1; Indels
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....TERISTICS:
....H: 197 amino acids
TYPE: amino acid
TOPOLOGY: 1:---
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Best Local Similarity 85.7
Matches 6; Conservative
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US-08-415-655-6
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                                                                                                                                         PARCHIA NO. 9.203502
APPLICANT: BILERS, MARTIN
APPLICANT: BILERS, MARTIN
APPLICANT: BILERS, MARTIN
APPLICANT: BUBRGIA, ANDREA
APPLICANT: SEDLAGEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
CURRENT APPLICATION NUMBER: 197 809/215,221
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 197 56 975.7
PRIOR APPLICATION NUMBER: 197 56 975.7
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PREHEIN Ver. 2.1
SEQ ID NO 52
LENGTH: 194
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Sequence 54, Application US/0921521
Patent No. 6565562
GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BUERGIN, ANDREA
APPLICANT: BUERGIN, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
TITLE OF INVENTION: INHIBITIORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026083/0192
CURRENT APPLICATION NUMBER: 197 56 975.7
PRIOR APPLICATION NUMBER: 197 56 975.7
NUMBER OF SEQ ID NOS: 57
SOFTHARE: PATENT NOS: 57
NUMBER OF SEQ ID NOS: 57
SOFTHARE: PATENT NOS: 21
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85.7%; Pred. No. 8.4;
tive 0; Mismatches 1; Indels
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Pred. No. 8.4;
0; Mismatches 1; Indels
                                                                                 US-09-215-221-52
; Sequence 52, Application US/09215221
; Patent No. 6265562
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US-09-215-221-54
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Best Local Similarity 85.7
Matches 6; Conservative
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66 LEGRYEW 72
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Murine sp. FEATURE:
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US-08-275-983B-2
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LENGTH: 195
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TYPE: PRT
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Batent No. 6025480
GENERAL INFORMATION:
GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE 
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Sequence 2, Application US/08275983B
Patent No. 568865
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Roberts, James M.
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: 180lated p27 Protein, Nucleic Acid Molecules
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS.
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 197;
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CONTINE: COLUMN COLUMN CONTINE: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppodish
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 13.58P-1994
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US 08/179,045
FILING DATE: VOT-JAN-1994
ATTORNEY/AGRAT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
RELECOMMUNICATION INFORMATION:
TELEPRATION FOR SEQ ID NO:
TELEPRATIC (617)227-7400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13.7 aning acids
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Pred. No. 8.5;
0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 4, Application US/08794002
Patent No. 6316208
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TYPE: amino acids
TYPE: amino acid
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                                                                                                                                                                                                     Query Match
Best local Similarity 85...
6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                      70 LEGRYEW 76
                                                                                                                                                                         ) ORGANISM: Murine sp. US-09-215-221-57
                                                                                                                                                                                                                                                                           2 LXGRYEW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One P
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US-08-794-002-4
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0
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Patent No. 6245965

GENERAL INFORMATION:
APPLICANT: ROUSSEL MARTINE F.
APPLICANT: SINDY, FREDERIQUE
APPLICANT: ZINDY, FREDERIQUE
APPLICANT: CUNNINGHAM, JUSTINE
TITLE OF INVENTION: CELLS THAT LACK P191NK4D AND P27KIP1 ACTIVITY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 1340-1-025
CURRENT APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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85.7%; Pred. No. 8.5;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 3; Length 197;
Pred. No. 8.5;
0; Mismatches 1; Indels
Sequence 57, Application US/09215221
Patent No. 6265562
GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BURBGIN, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
                                                                                                                                                                         TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYRE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                  92.5%;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-240-906-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                70 LEGRYEW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LXGRYEW 8
                                                                                                                                                                                                                                                                                                                                                                                                                            2 LXGRYEW 8
                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO
US-08-415-655-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-215-221-57
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TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF FILE REPERENCE: 0260813/012 CURRENT APPLICATION NUMBER: US/09/215,221 CURRENT FILING DATE: 1998-12-18 PRIOR FILING DATE: 1998-12-18 PRIOR FILING DATE: 1997-12-20 NUMBER OF SEQ ID NOS: 57 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 57 LENCTH: 197 TYPE: PRIOR FILING PATE: 197 TYPE: PRIOR FILING DATE: PRIOR FILING FILING PRIOR FILING FILIN .. ö Gaps Gaps .. 0 ö GENERAL INFORMATION:
APPLICANT: Roberts, James M.
APPLICANT: Porter, Peggy L.
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS
TITLE OF INVENTION: PRODUCTION AND USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: ONE POST Office Square Indels 1; Indels COUNTR: MAS

COUNTR: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,002

FILING DATE: 03-FEB-1997

CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REGISTRATION NUMBER: 36,709

REJERENCE/DOCKET UNMBER: 36,709

TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-832-1000

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENDOMATION FOR SEQ ID NO: 4: Score 37; DB 3; Pred. No. 8.5; 0; Mismatches 92.5%; Score 37; DB 3; 85.7%; Pred. No. 8.5; iive 0; Mismatches 1 2 LXGRYEW 8 8

70 LEGRYEW 76 g

us-09-574-735c-35.rai

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TYPE: PRT
CORGANISM: Mus musculus
US-09-483-597-8
                                                                                                                                                                                                                                                                        70 LEGRYEW 76
                                                                                                                                                                                                                           2 LXGRYEW 8
LENGTH: 197
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US-09-483-597-8
; Sequence 8, Application US/09483597
; Patent No. 6589505
; Patent No. 6589505
; Patent No. 6589505
; APPLICANT: ROUSEL, MARTINE F.
APPLICANT: ZINDY, FREDERIQUE
; APPLICANT: ZINDY, FREDERIQUE
; APPLICANT: CUNNINGHAM, JUSTINE
; APPLICANT: CUNNINGHAM, JUSTINE
; APPLICANT: CURNINGHAM, JUSTINE
; APPLICANT: CURNINGHAM, JUSTINE
; APPLICANT: CURNINGHAM, JUSTINE
; APPLICANT: SEGIL, NEIL
; APPLICANT: AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-025N
; CURRENT APPLICATION NUMBER: 06/117,719
; EARLIER FILING DATE: 1999-01-29
; WUMBER OF SEC ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEC ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                         GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Roff, Andrew
APPLICANT: Roff, Andrew
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS
TITLE OF INVENTION: PRODUCTION AND USE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSED: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STREET: MA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: STEEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,039B
FILING DATE: US-MAY-1997
MANNE: VALORE MAY-1997
MANNE: VALORE MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                    Sequence 4, Application US/08854039B
Patent No. 6355774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: MIV-
TELECOMMUNICATION INFORMATION:
TELEFONE: 617-832-1000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-854-039B-4
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                                               US-08-854-039B-4
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 92.5%; Score 37; DB 4; Length 197; 85.7%; Pred. No. 8.5;
                                      1; Indels
                                                                                                                                                                Search completed: October 26, 2004, 15:34:19 Job time: 13.2308 secs
Query Match
Best Local Similarity 85.7
Matches 6, Conservative
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92.5
37
14
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Sequence 55128, A
Sequence 14, Appl
Sequence 13, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
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                                                                                                                                                                                October 26, 2004, 15:19:44; Search time 115.077 Seconds (without alignments) 22.507 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

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10: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB_pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-767-701-55128

US-10-451-139-13

5 US-10-451-139-13

5 US-10-688-291-4

5 US-10-451-139-21

5 US-10-421-339-21

5 US-10-333-006-11

5 US-10-333-006-12

US-09-733-507-2

US-09-733-507-2

US-09-733-507-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1364641 seqs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                          US-09-574-735C-35
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                                                                                                                                                                                                                                                                                                                                              1 XLXGRYEW 8
                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
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                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
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Sequence 11, Appl Sequence 153517, Sequence 2, Appli Sequence 1, Appl Sequence 2, Appli Sequence 4, Appli

92.5 205 15 US-10-424-599-18228 Sequence 182928, 92.5 225 16 US-10-437-953-19874 Sequence 198574, 92.5 245 13 US-10-087-122-1161 Sequence 198574, 92.5 245 13 US-10-087-122-1161 Sequence 36263, Pp. 90.0 218 16 US-10-767-711-3623 Sequence 36263, Pp. 90.0 228 15 US-10-424-599-235800 Sequence 128205, Pp. 0 223 15 US-10-688-211-6 Sequence 6, Appliance 10.0 223 15 US-10-425-114-5918 Sequence 6, Appliance 10.0 225 15 US-10-156-764-17900 Sequence 5738, Pp. 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	ALIGNMENTS Application US/10333006 5. US20040019926A11 Frankard, Valerie Marie-No. US20040019926A111e sperse Borca, Adrian Marius Droual, Anne-Marie Mironov, Vladimir Harz, Lb. rk Harz feld, Yves Mironov, Vladimir Harz feld, Yves ENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE IN CE: 1187-13 CE: 1187-13 ATTON NUMBER: US/10/333,006 NG DATE: 2003-01-14 ATTON NUMBER: US 60/218,471 DATE: 2000-10-13 O ID NOS: 59 Lentin Version 3.1	milarity 95.0%; Score 38; DB 15; Length 53; Conservative 0; Mismatches 1; Indels 0; Gap. XCRYEW 8 SGRYEW 48
4 5 6 7 8 9 0 1 1 5 1 1 4 1 1 6 7 8 9 0 1 1 5 1 1 4 1 1 1 1 7 8 9 0 1 1 5 1 1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1	T. 1 T. 1 T. 1 T. 1 T. 1 T. 233.006-17 T. 206-17 T. 206-18 T. 206-18	Query Match Best Local Simila Matches 6; Cc 2 LXGRY
	RESULT US-10 Seque REBLE APPR APPR APPR APPR APPR APPR APPR APP	Ques Best Matc

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; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; CURRENT SPERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR APPLICATION NUMBER: WG 60/255,908
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; RIGHT FILING DATE: 2000-12-18
; SOFTWARE: PATENTING NUMBER: US 60/255,908
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 13
; LEWOTH: 137
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-13
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Publication No. US20040098763A1
GENERAL INFORMATION:
APPLICANT: WANG, HONG
APPLICANT: WANG, HONG
APPLICANT: HOWE, HONG
APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
APPLICANT: HER MAJESTY IN RIGHT OF CANADA
APPLICANT: HER MAJESTY IN RIGHT OF CANADA
APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 4810-62237
CURRENT APPLICATION NUMBER: WO PCT/CA01/01825
PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-668-291-4
| Sequence 4, Application US/1068291
| Sequence 4, Application US/1068291
| Publication No US20040073969A1
| GENERAL INFORMATION:
| APPLICANT: De Valeider, Lieven
| APPLICANT: Landrieu, Isabelle
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
| TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
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Pred. No. 18;
0; Mismatches 1
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%;
85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                          APPLICANT: Kovalic, David K.
APPLICANT: Sovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Caco, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
LENGTH: 132
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Sequence 14, Application US/09733507

Patent No. US20010025379A1

GENERAL INFORMATION:
TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
TITLE OF INVENTION: Regulators
FILE REFERENCE: 81601-3

CURRENT APPLICATION NUMBER: US/09/733,507

CURRENT FILING DATE: 1090-12-02

PRIOR APPLICATION NUMBER: CA 2,256,121

PRIOR PILING DATE: 1990-12-31

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 14

LENGTH: 137
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) Publication No. US20040098763A1

CENERAL INFORMATION:
APPLICANT: WANG, HONG
APPLICANT: EOWEX, LARRY C.
APPLICANT: HEN WAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
APPLICANT: ARAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
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Pred. No. 17;
0; Mismatches 1; Indels
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US-10-767-701-55128
                                                                                                                                        Sequence 55128, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-09-733-507-14
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6, Conservative
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ORGANISM: Sorghum bicolor
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                                                                              RESULT 2
US-10-767-701-55128
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US-10-451-139-13
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US-09-733-507-14
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Sequence 153517, Application US/10424599
| Sequence 153517, Application US/10424599|
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongwei
| APPLICANT: Cao Yongwei
| APPLICANT: Cao Yongwei
| APPLICANT: APPLICANT: APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION NUMBER: US/10/424,599
| CURRENT APPLICATION NUMBER: US/10/424,599
| NUMBER OF SEQ ID NOS: 285684
| SEQ ID NO 153517
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Facent No. US20010025379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
TITLE OF INVENTION: Regulators
TITLE OF INVENTION OF REGULATORS
CURRENT APPLICATION NUMBER: US/09/733,507
CURRENT FILING DATE: 2000-12-02
FRIOR APPLICATION NUMBER: CA 2,256,121
FRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 191
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                                                                                                                                                                DB 15; Length 22; 5.4;
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Pred. No. 11;
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US-10-424-599-153517
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                                                                                                                                                                          Score 37; DB Pred. No. 5.4; 0; Mismatches
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                     version 3.1
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn versic
SEQ ID NO 11
LENGTH: 22
                                                                                                            ; ORGANISM: Oryza sativa
US-10-333-006-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
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Publication No US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Cap Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 210190
LENGTH: 224
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APPLICANT: Prankaria Adrian Marius
APPLICANT: Droual, Anne-Marie
APPLICANT: Mironov, Vladimir
APPLICANT: Mironov, Vladimir
APPLICANT: Mironov, Vladimir
APPLICANT: Hatzfeld, Yves
FILE REPERBUCE: 1187-13
CURRENT APPLICANTION NUMBER: US/10/333,006
CURRENT APPLICANTION NUMBER: US/10/333,006
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Pred. No. 27;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: PCT/1B01/01492
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR PILING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
                              60/255,908
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Publication No. US20040019926A1
GENERAL INFORMATION:
    PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
LENGTH: 222
                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-21
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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US-10-424-599-210190
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US-10-333-006-11
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Sequence 4, Application US/09865018
Patent No. US20020110886A1
GENERAL INFORMATION:
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Matches 6, Conservative
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US-09-865-018-4
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Sequence 2, Application US/10451139
Publication No. US20040098763A1
GENERAL INFORMATION:
APPLICANT: MANG, HONG
APPLICANT: APPLICANT: POWGK, LARRY C.
APPLICANT: FOWEK, LARRY C.
APPLICANT: FOWEK, LARRY C.
APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
TITLE OF INVENTION UNDER: US 10/451,139
CURRENT FILING DATE: 2003-06-18
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,908
PRIOR FILING DATE: 2000-12-18
SPIOR FILING DATE: 2000-12-18
SOFTWARE: PALENTIN VET. 2.0
SOFTWARE: PALENTIN VET. 2.0
                                                                                                                                                                Sequence 10, Application US/09733507

Patent No. US2001025379A1

APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth TITLE OF INVENTION: Regulators

TITLE OF INVENTION: Regulators
FILE REFERENCE: 81601-3

CURRENT FILING DATE: 2000-12-02

PRIOR APPLICATION NUMBER: US/09/733,507

PRIOR APPLICATION NUMBER: CA 2,256,121

PRIOR PILING DATE: 1998-12-31

NUMBER OF SEC ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 191
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85.7%; Pred. No. 36;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.5%; Score 37; DB 9; Length 191;
85.7%; Pred. No. 36;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
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TYPE: PRT
: ORGANISH: Arabidopsis thaliana
US-10-451-139-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                          181 LEGRYEW 187
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                  2 LXGRYEW 8
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US-09-733-507-10
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US-10-451-139-2
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RESULT 13

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GREEAL WESTONGINGSEAN CORRECTION AND USE CREATER AND METHOD FOR ITS TITLE OF INTENTION COMPANDATION COMPANDATION CONTRICT AND USE CREATER AND METHOD FOR ITS COMPANDATION COMP
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sequence 198574, Application US/10437963
; Sequence 198574, Application NS/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Would K.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198574
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                                                                                            Query Match 92.5%; Score 37; DB 15; Length 205; Best Local Similarity 85.7%; Pred. No. 38; Matches 6; Conservative 0; Mismatches 1; Indels
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pep
US-10-424-599-182928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT4530_9421C.1.pep
US-10-437-963-198574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 26, 2004, 15:33:29 Job time: 115.077 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 LOGRYEW 209
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                                                                                                                                                                                                   2 LXGRYEW 8
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US-10-437-963-198574
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 26, 2004, 15:27:13 ; Search time 11.0769 Seconds (without alignments) 69.490 Million cell updates/sec

US-09-574-735C-35 40 1 XLXGRYEW 8 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summarles

PIR 79:*
1: Dirl:*
2: DirZ:*
3: DirA:*
4: DirA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

201	Description	(1)	cyclin-cdk inhibit		뎏.	hypothetical prote	6	hypothetical prote	hypothetical prote		gene p27Kip1 prote		hypothetical prote	<u>а</u>	chrome-	membrane	Кe	(1)	valine-tRNA ligase	TonB-dependent rec	hypothetical prote	porin O precursor	й	tein - Le	i] W aspholipase A [i	hypothetical prote	probable esterase	ical	entenylt	hypothetical prote
SUMMERTES	Δ	0113	90	C83587	1027	A75022	T36265	600	653	T09968	152718	T46140	G83487	S63401	QRECFE	B85499	B90648	AI3197	SYBSVS	B87270	T23957	A82820	F83400	m	AB0467	T00797	7096	8	9	9510
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	Length																											461		73
٠	Query Match	! .:	٠.	92.5	~		87.5					'n	ı'n.	i	10		'n	85.0	'n	'n,	82.5	N.	ď	0	ö	0	ö	80.0	0	7
	Score			37	36	35	35	3.4	34	34	34	34	34	34	34	3.4	34	34	34	34	33	33	33	32	32	32	32	32	32	31
	Result No.		8	m	4	ľ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote T-cell receptor V- T-cell receptor al	probable integral probable flavodoxi		hypothetical prote hypothetical prote hypothetical prote	·++!	hypothetical prote probable lipo prot gene 10 protein -
A97975 S40138 RWHIIAA	H81823 F71263	C82629 H86026 F91180	A82627 H71208 G82378	S47756 H84060	C70194 E70914 S34955
00 00	100	7 77 79	210	100	000
113 113	1 T T T T T T T T T T T T T T T T T T T	178	195 217	24.2 24.2 0.0 0.0	355 4 20 7 20
77.5	2.77	77.5	77.5	77.5	77.5 77.5
337	1 1 1 1 1	7 F F	311	3 8 8	311
30	0 W W 0	 	. w w c	4 4 4 5 4 4	44 45 5

ALIGNMENTS

_	RESULT 1
	T01132
	cyclin-dependent kinase inhibitor protein [imported] - Arabidopsis thaliana
	N'Alternate names: hypothetical protein F26B6.8
_	C.Species: Arabidopsis thaliana (mouse-ear cress)
	C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
	C;Accession: T01132; F84624
_	R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
_	submitted to the EMBL Data Library, June 1998
_	A; Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
_	A; Reference number: Z14198
	A; Accession: T01132
	A;Status: translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
	A; Residues: 1-191 < ROU>
	A; Cross-references: UNIPROT: 082809; EMBL: AC003040; NID: 93242700; PID: 93242706
	A;Experimental source: cultivar Columbia
	Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fulli, C.Y.;
	M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
	euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
_	Nature 402, 761-768, 1999
_	A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
	A; Reference number: A84420; MUID: 20083487; PMID: 10617197

A;Reference number: A84420; MUD:20083487; FMLD:1001/137,
A;Accession: F84624
A;Atcession: F84624
A;Atatus: preliminary
A;Molecule type: DNA
A;Residues: L-191 < 870>
A;Crose-references: GB:AE002093; NID:g3242706; PIDN:AAC23758.1; GSPDB:GN00139
A;Genetics: F26B6.8; At2g23430
A;Genetics: P666.8; At2g23430
A;Mon position: 2
A;Introns: 66/3; 81/2; 170/2

Gaps ·. Ouery Match

92.5%; Score 37; DB 2; Length 191;
Best Local Similarity 85.7%; Pred. No. 3.6;
Matches 6; Conservative 0; Mismatches 1; Indels

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181 LEGRYEW 187 2 LXGRYEW 8 a ð

RESULT 2 I49064

cyclin-cdk inhibitor p27 - mouse
cyclin-cdk inhibitor p27 - mouse
NyAlexnate names: CDI p27; G1 cyclin-cyclin-dependent kinase inhibitor p27
Syspecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: I49064
E;Accession: I49064
E;Tyoyoshima, H.; Hunter, T.
Cell 78, 67-74, 1994
A;Title: p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, is related to

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C;Accession: A75022
R;anonymous, Genoscope
Rubmitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-216 «KAW»
A, Cross-references: UNIPROT: Q9UXZ7; GB: AJ248288; GB: AL096836; NID: 95458960; PIDN: CAB5061
A, Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-565 <MUR>
A,Cross_references: UNIPROT: Q9WX17; EMBL:AL079345; PIDN:CAB45351.1; GSPDB:GN00070; SCOED
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C;Superfamily: bifunctional uroporphyrin-III C-methyltransferase/uroporphyrinogen-III sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable uroporphyrin-III C-methyltransferase / uroporphyrinogen-III synthase - Streptom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SCC22.15c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004 C; Date: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004 R; Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, July 1999 A; Recence number: Z21574 A; Recence number: Z21574 A; Accession: T36005 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                      lypothetical protein PAB1224 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.5%; Score 35; DB 2; Length 216; Best Local Similarity 71.4%; Pred. No. 10; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2; Length 565;
Pred. No. 28;
1; Mismatches 1; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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A;Accession: T36265
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137 IAGRYEW 143
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334 VTGRYEW 340
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53 MRGRYEW 59
                2 LXGRYEW 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: PAB1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein PA0462 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-29-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83587
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathota; Reference number: A82950; MUID:20437337; PMID:10584043
A;Reference number: A82950; MUID:20437337; PMID:10584043
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-234 cSTO>
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0462
A;Reference number: A54839; MUID:94306519; PMID:8033213
A;Accession: 149064
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-197 <RES>
A;Residues: 1-197 <RES>
A;Cross-references: UNDROOT:P46414; EMBL:U10440; NID:9532771; PIDN:AAA21149.1; PID:95327
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-ibulose-phosphate 4-epimerase (EC 5.1.3.4) [imported] - Yersinia pestis (strain CO92) (.Species: Yersinia pestis (C.5pecies: Yersinia VI) (C.5pecies: Yersinia Yorkin VI) (C.5pecies: Yersinia Y
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                                                                                                                                                                                                                                                                                                       Score 37; DB 2; Length 197;
Pred. No. 3.8;
0; Mismatches 1; Indels
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90.0%; Score 36; DB 2; Length 231;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels
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A;Gene: arab
C;Superfamily: L-ribulose-phosphate 4-epimerase
C;Keywords: isomerase
                                                                                                                                                                                                                                                                                                                       92.5%;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 LEGRYEW 76
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Cispefies: Homo sapiens (man)
Cispefies: Homo sapiens (man)
Cispefies: Homo sapiens (man)
Cispefies: Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
Cispefies: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
Cispefies: 01-182718
Airitle: Assignment of the human p27Ripl gene to 12pl3 and its analysis in leukemias.
Airitle: Assignment of the human p27Ripl gene to 12pl3 and its analysis in leukemias.
Aireference number: 152718; MUID:95188144; PMID:7882309
Airitle: Assignment of the human p27Ripl gene to 12pl3 and its analysis in leukemias.
Aireference number: 152718; MUID:95188144; PMID:7882309
Airitle: Airitle: Assignment of the human p27Ripl gene to 12pl3 and its analysis in leukemias.
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Airitle: Assignment of the human p27Ripl gene to 12pl3 and its analysis in leukemias.
Airitle: Assignment of th
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T46140

Typotherical protein T3A5.10 - Arabidopsis thaliana

(Species: Arabidopsis thaliana (mouse-ear cress)

C)Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C)Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C)Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

R)Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

R)Bloccker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, F.; Salsubmitted to the Protein Sequence Database, December 1999

A)Reference number: 223024

A)Accession: T46140

A)Accession: T46140

A)Accession: T46140

A)Accession: T46140

A)Accession: T46140

A)Accession: T46140

A)Accession: C: Quetier, F.; Salsubmitary

A)Accession: C: Quetier, F.; Salsubmitary

A)Accession: T46140

A)Accession: T4
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(98348.7)

Hypothetical protein PA1268 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Species: Pseudomonas aeruginosa

C;Dates: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Jaccession: G848.7

R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
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                                              Indels
                                                   ;
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Pred. No. 15;
1; Mismatches
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Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%;
71.4%;
    71.48;
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A;Introns: 109/3; 130/2; 186/2
A;Note: T3A5.10
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5; Conservative
                                                   5; Conservative
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Best Local Similarity
...hea 5; Conserv?
                                                                                                                                                                                                185 LKGRYDW 191
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                   2 LXGRYEW 8
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A;Introns: 159/1
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Best Local S
Matches 5
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C;Species: Chenopodium rubrum (red goosefoot)
C;Species: Chenopodium rubrum (red goosefoot)
C;Accession: T09968
R;Fountain, M.D.; Renz, A.; Beck, E.
Submitted to the EMBL Data Library, November 1997
A;Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic A;Reference number: Z16910
A;Accession: T09968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypotherical protein F14J22.14 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Yri, Liu, X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, T.; Lin, T.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:g10120423; PIDN:AAG13048.1; GSPDB:G
         A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-144 < CSED>
A; Residues: 1-144 < CSED>
A; Cross-references: UNIPROT: 09XAC3; EMBL: AL096839; PIDN: CABS0758.1; GSPDB: GN00070; SCOED
A; Experimental source: strain A3(2)
A; Genetics:
A; Genetics:
A; Genetics: CCSDB: SCC22.15c
C; Superfamily: Streptomyces coelicolor hypothetical protein SCC22.15c
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C,Genetics: A;Genet. Source: photoautotrophic cells derived from hypocotyl tissue A;Gene: CDXII
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 15;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 196;
                                                                                                                                                                                                                                                                                                                                                                Length 144;
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A;Molecule type: mRNA
A;Residues: 1-196 <FOU>
A;Cross-references: UNIPROT:048597; EMBL:AJ002173
                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches
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Best Local Similarity 71.4
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
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C, Genetics

RESULT 9

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M.J., B K., Lim

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A;Molecule type: DNA
A;Residues: 723-747 <BUR>
A;Cross-references: EMBL:X05810
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482 LGGRYDW 488
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A;Molecule type: DNA
A;Residues: 1-747 <STO>
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A;Map_position: 4 min
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C;Species: Escherichia coli
C;Species: Salas, A25196; Z45219; S06358
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Bhao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64738
A;Accession: F64738
A;Accession: F64738
A;Accession: F6438
A;Accession: F6438
A;Accession: F6438
A;Accession: Cameron
A;Molecule type: DNA
A;Residues: 1-47 < Cameron
A;Molecule type: DNA
A;Residues: UNIPROT:P06971; GB:AE000124; GB:U00096; NID:91786339; PIDN:AAC73261.
A;Experimental source: strain K-12, substrain MG1655
A;Title: Protein fusions of beta-galactosidase to the ferrichrome-iron receptor of Bsche
A;Reference number: A25196; MUID:86085668; PMID:3079747
                                                                                                                                                                                                      A; Accession: GB348/
A; Status: preliminary
A; Status: preliminary
A; Status: Dreliminary
A; Status: Dreliminary
A; Residues: 1.314 c8T0>
A; Cross.references: UNIPROT:091476; GB:AE004556; GB:AE004091; NID:g9947194; PIDN:AAG0465
A; Cross.references: UNIPROT:091476; GB:AE004556; GB:AE004091; NID:g9947194; PIDN:AAG0465
C; Ganetics:
A; Gene: PA1268
C; Superfamily: proline racemase
C; Superfamily: proline racemase
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
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Cyperces 53401
Cyccession: 563401
Cyccession
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Pred. No. 38;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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LRGKYEW 473
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A, Description: located in the outer membrane, binds the ferrichrome-iron ligand; interac
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: B85499

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-608, RP', 611-747 <FUJ>
A; Residues: 1-608, RP', 611-747 <FUJ>
A; Residues: 1-608, RP', 611-747 <FUJ>
A; Cross-references: EMBL:D26562; NID:g473770; PIDN:BAA05598.1; PID:g473809
A; Experimental source: strain K-12, substrain W3110
B; Burkhardt, R.; Braun, V.
A) Genet. 209, 49-55, 1987
A; Fitle: Nucleotide sequence of the fhuc and fhub genes involved in iron (I A; Reference number: A32650; MUID:88038363; PMID:2823072
A; Accession: S06358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: iron transport; membrane protein
E;1-33/Jonain: signal sequence #status predicted <SIG>
F;1-33/Jonain: signal sequence #status predicted <SIG>
F;8-7-35/Domain: ferrichrome-iron receptor #status predicted <MAT>
F;88-235/Domain: tonB-dependent receptor amino-terminal homology <TNC>
F;468-747/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
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A;Accession: A25196
A;Molecule type: DNA
A;Residuse: 1-609, 'RP', 611-747 <COU>
A;Cosiduse: 1-609, 'RP', 611-747 <COU>
A;Coss-references: GB:D26562; NID:9473770; PIDN:BAA05598.1; PID:9473809
A;Experimental source: strain K-12
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                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, January 1994 A;Reference number: 845181 A;Accession: 845219
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Search completed: October 26, 2004, 15:40:08 Job time : 13.0769 secs

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Gétzzz glycine max
Gégwc3 anas platyr
G8jiv2 gallus gall
Aas12099 anas plat
Aas1275 glycine m
Gétzz3 glycine m
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Aas13377 glycine m
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Aas13376 glycine m
O04154 arabidopsis
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Q9fs28 pisum sativ
P46414 mus musculu
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Q6t2z2 glycine max
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035792 rattus norv
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                                                 ; Search time 44.6154 Seconds (without alignments) 103.171 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                 1825181 segs, 575374646 residues
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Q9FKBS
Q99V92
Q6T220
Q6T221
AAS13377
Q6T221
AAS13376
Q04154
Q8LDX1
Q8LDX1
Q9FS28
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Maximum Match 100%
Listing first 45 summaries
                                 protein search, using sw model
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AAS02099
AAS13375
Q6T2Z3
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Q91656
Q8DJR3
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Q8GT29
Q8ZEE3
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Q8D0J2 AAS62245 Q9CN07 Q6PV56

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99uxz7 pyrococcus
Q6dt6 erwinia car
Q6dt6 erwinia car
Q9wx17 streptomyce
Q8ceff homo sapien
Q8ceff homo sapien
Cace2381 homo sapien
Cace3281 homo sapien
Q9xg nicotiana s
Q43806 homo sapien
Q9beas scrota
Aas89651 yersinia
                                                  CDNB MUSVI
   Q9UXZ7-
Q6D5T0
Q9WX17
Q8ZE75
Q9CAF4
Q8XX31
Q708Y31
Q708Y31
Q708Y31
Q708Y31
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09BEA5
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ALIGNMENTS

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                                                                                                                Dycopersicon esculentum (Tomato).

Bukaryota; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                             Bibls B., Joubes J., Hernould M., Inze D., Raymond P., Chevalier C., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, A444125; CAD29469-1; -..

EMBL, A444125; CAD29469-1; -..

GO, GO:0004861; E:cyclin-dependent protein kinase inhibitor a. ..; IE GO, GO:0007068; E:cyclin-dependent protein kinase inhibitor a. ..; IE InterPro; IPR003175; CDI.

InterPro; IPR003175; CDI.

SEQUENCE 185 AA; 21189 MW; 48DCC89A5336C676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-07-2004 (TrEMBLrel. 28, Last annotation update)
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24G6 (Cyclin-dependent kinase inhibitor 3).
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                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 AA.
                         185 AA
                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 38; DB 85.7%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                        Created)
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                          PRT;
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SEQUENCE FROM N.A.
MEDLINE=98403884; PubMed=9734815;
                                     vi-wAR-2003 (TrEMBLrel. 23, C1 01-WAR-2003 (TrEMBLrel. 23, La 01-OCT-2003 (TrEMBLrel. 25, La P27KIP1-related-protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 LSGRYEW 180
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Locular,
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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Q9FKB5
RESULT 1
            QBGT28
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us-09-574-735c-35.rup

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PRELIMINARY;
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                            Glycine max (Soybean)
                                                 152 LEGRYEW 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 LEGRYEW 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 AA;
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       LXGRYEW
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NON TER 166
SEQUENCE 166
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                                                                                                                                                                                                                                                                                             Plant Cell 13:1653-1668(2001).

Plant Cell 13:1653-1668(2001).

BMBL; AB01242; BAB09455.1; -

BMBL; AJ01554; CAC41617.1; -

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . ; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0007050; P:cell cycle arrest; IEA.

InterPro; IPR003175; CDI.

Pfam; PF02234; CDI: 1.
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MEDLINE=22369088; PubMed=12481070;
Jasinski S., Perennes C., Bergounioux C., Glab N.;
"Comparative Molecular and Functional Analyses of the Tobacco Cyclindependent kainase inhibitor NkKISia and its spliced variant NtKISIb.";
Plant Physiol. 130:1871-1882 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CDK/cyclin inhibitor.
Name=kisla; Synonyms=kisl;
Nicotiana tomentosiformis (Tobacco).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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SEQUENCE FROM N.A.
MEDLINE=21342510; PubMed=11449057;
de Veylder L., Beeckman T., Beemster G.T.S., Krols L., Terras F.,
Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.;
"Functional analysis of Cyclin-dependent kinase inhibitors of Arabidopsis.";
Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grondard S., Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ297904; CAC82733.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004631; E:Cyclin-dependent protein kinase inhibitor a.

GO; GO:0007050; E:Cyclin-dependent protein kinase inhibitor a.

InterPro; IPR003175; CDI.

Ffam; PF02224; CDI; 1.

SEQUENCE 163 AA; 18301 MW; E154AS9D491E66B7 CRC64;
                                  "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned PI and TAC clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h Similarity 85.0%; Score 38; DB 2; Length 222; Similarity 85.7%; Pred. No. 14; 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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NCBI TaxID=4098;
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10033V92
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DT 01-DD
DT 01-DD
DT 02-DD
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10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor 2;2 (Fragment).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Li S., Reverdatto S., Nielsen N.C.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY430104; AAS13377.1; -.
GO; GO:0016301; F:kinase activity; IEA.
InterPro; IPR003175; CDI.
InterPro; IPR03345 CDI.
Oyclin; Kinase 166
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Li S., Reverdatto S., Nielsen N.C.;
"CDNA of cell-cycle genes in soybean cotyledons.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, Ay439104; AAS13377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;
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18850 MW; 40FB19CF72A8A640 CRC64;
05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor 2/2 (Fragment).
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GTRAIN=Columbia;
MEDLINE=9724401;
Wheng H., Fowke L.C., Crosby W.L.;
Wang H., Fowke L.C., Crosby W.L.;
Wang H., Fowke L.C., Crosby W.L.;
Wang H., Fowke L.C., Crosby W.L.;
Wature 386:451-452(1997).
Nature 386:451-452(1997).
Nature 386:451-452(1997).
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
GO; GO:0004861; F:kinase activity; IEA.
GO; GO:00016301; F:kinase activity; IEA.
InterPro; IPRO03175; CDI.
Pfam; PF02224; CDI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ICK1; Synonyms=At2g23430;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang H., Qi Q., Schorr P., Cutler A.J., Crosby W.L., Fowke L.C.; "ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis thallana interacts with both Cdc2a and CycD3, and its expression is induced by abscisic acid."; plant J. 15:501-510(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
Rounsley S.D., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Town C.D., Kaul S.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF0039640; AAC23758.1; -.

EMBL; AF019587; AAC34660.1; -.

PIR; T01132; T01132.

GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0007060; P:cell cycle arrest; IBA.

FILEFPC; IPR003175; CDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 191
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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Pred. No. 20;
0; Mismatches
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MEDLINE=98426383; PubMed=9753775;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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SEQUENCE 191
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082809
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                                                                                                                                          Glycine max (Soybean).

Bukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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Pred. No. 19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 2; Length 180;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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Li S., Reverdatto S., Nielsen N.C.;
Lio S., Reverdatto S., Nielsen N.C.;
"CDNA of cell-cycle genes in soybean cotyledons.";
Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY439103; AAS13376.1;
                                                                                                                                                                                                                                                               20060 MW; 9E4ABBF0918246E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      20060 MW; 9E4ABBF0918246E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor 2;1 (Fragment).
Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04, Created)
04, Last sequence update)
24, Last annotation update)
inhibitor protein.
                                                                    05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor 2;1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AA
                                 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                   PRT;
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Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.5%;
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01-JUL-1997 (TEMBLE). 04
01-JUL-1997 (TEMBLE). 04
01-JUN-2003 (TEMBLE). 24
Cyclin-dependent kinase ir
Name=ICK1;
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180 AA; 200
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                  NCBI_TaxID=3847;
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10-MAY-2004
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10-MAY-2004
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197 AA

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STRAIN=FV9/N; TISSUB=Salivary gland;

KELINE=21886227; Pubmed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Halte S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Matching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
TISSUE-Axillary bud;
Shimizu-Sato S., Mori H.;
Submizu-Sato S., Mori H.;
Submizu-Sato S., Mori H.;
Submizued (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029483; BAB20660.1; ~.
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. ..; IEA.
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. ..; IEA.
GO; GO:0007050; F:coll cycle arrest; IEA.
GO:0007050; PR003175; CDI.
Pfam; PF02234; CDI; 1.
Cyclin; Kinase.
SEQUENCE 192 AA; 21921 MW; E76D734000885EBZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toyoshima H., Hunter T.; "p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, related to p21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M. Tempst P., Massague J.; "Cloning of p57Kipl, a cyclin-dependent kinase inhibitor and a potential mediator of extracellular antimitogenic signals."; Cell 78:59-66(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NCV-1995 (Rel. 32, Created)
01-NCV-1995 (Rel. 32, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%; Score 37; DB 2; Length 192; 85.7%; Pred. No. 20; ive 0; Mismatches 1; Indels
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MEDLINE=94306519; PubMed=8033213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=94306518; PubMed=8033212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor p27) (p27Kip1). Name=Cdknlb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related to p21.";
Cell 78:67-74(1994).
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Best Local Similarity
Matches 6; Conserv
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P46414;
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CDNB MOUSE
                SKARDBRRRRS
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BECOVER V. Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

ENEL, ANSO5749; AAM625967.1; -.
GO, GO:0005349; C:nucleus; IEA.
GO, GO:00046319; F:cyclin-dependent protein kinase inhibitor a. ..; IEA.
GO, GO:00016301; F:kinase activity; IEA.
GO, GO:0007050; P:cell cycle arrest; IEA.
InterPro; IPRO03175; CDI.
Pfam: PF02234; CDI: 1.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last amontation update)
01-0Th-2003 (TrEMBLrel. 24, Last amontation update)
Cyclin-dependent Kinase inhibitor protein.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota, Viridiplantae; Etreptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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MEDLINE=2208475; PubMed=12093376;
Haas B.J., Volfcvsky N., Town C.D., Troukhan M., Alexandrov N. Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
                                                                                                Score 37; DB 2; Length 191;
Pred. No. 20;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.5%; Score 37; DB 2; Length 191;
85.7%; Pred. No. 20;
iive 0; Mismatches 1; Indels
                                       22283 MW; 0477A91E277C46B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AA; 22282 MW; 19B7A91E277C46B2 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyclin dependent kinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AA
                                                                                                   92.5%; Score 37;
85.7%; Pred. No. ;
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                                                           Query Match
Best Local Similarity 85.75,
Best Tocal 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                       181 LEGRYEW 187
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                                       191 AA;
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NCBI TaxID=3702;
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   Cyclin; Kinase.
SEQUENCE 191
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Q9FS28;
01-MAR-2001 (
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RESULT 10
028LDXI
AC Q8LDXI
AC Q8LDXI
DT 01-0C
DT 01-0C
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DT 01-0C
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SEQUENCE Query Match

RESULT 11 Q9FS28

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.

SEQUENCE FROM N.A

NCBI_TaxID=3888;

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. .; IEA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       | Managa R., Komori H., Ohtani K., Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. | Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. | EMBL; D86924; BAA19960.1; -. | EMBL; A7613194; AAT46041.1; -. | EMBL; A7623024; AAT46051.1; -. | EMBL; A7623040; AAT46051.1; -. | EMBL; A7620040; AAT46051.1; -. | EMBL; A762040; AAT46051.1; AAT46051.1; AAT46051.1; AAT46051.1; AAT46051.1; AAT46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawly, TISSUE-Spleen,
MEDLINE=97361761, PubMed=9218722,
MEDLINE=97361761, PubMed=9218722,
MCDUINE=97361761, PubMed=9218722,
"Cloning and characterization of rat p27Kip1, a cyclin-dependent kinase inhibitor.",
kinase inhibitor.",
EMBL: D83792, BAA21561.1,
HSSP, P46527, 1UGU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.
GO; GO:0007650; P:cell cycle arrest; IEA.
InterPro; IPR003175; CDI.
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85.7%; Pred. No. 21;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 197;
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                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       Dastvan F., Reidy M.A.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02234; CDI; 1. -- SF738078C2D555B2 CRC64; RENUENCE 197 AA; 22112 NW; 55738078C2D555B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 AA; 22139 MW; 55738078C2C9847F CRC64;
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Last annotation update)
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  through the MAP kinase signaling pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%; Score 37; DB
85.7%; Pred. No. 21;
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85.
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                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
                                                                                                        Uehara Y.;
Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEGRYEW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 LEGRYEW 76
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Best Local Similarity
Matches 6; Conserv
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                              Oncogene 0:0-0(0).
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                                                                                                                                                                                   SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMED cutstation the Buropean Bioinformatics Institute. There are DESTRICTIONS ON its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle; Nuclear protein; Protein kinase inhibitor.
DOWAIN 153 169 Nuclear localization signal (Potential).
WUTPAGEN 90 90 78 ->6: Loss of interaction with NUPSO.
SEQUENCE 197 AA; 22210 MW; 2D19A6CFEGEA650D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattuš norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                           EMBL; U10440; AAA21149.1; -.

R EMBL; U0968; AAA22235.1; -.

R EMBL; BC014296; AAH14296.1; -.

R EMBL; BC014296; AAH14296.1; -.

R HSSP; P46527; 1JSU.

R MGD; MG1:04565; Cdkn1b.

R GO; GC:0000515; F:protein binding; IPI.

R GO; GC:0005515; F:protein binding; IPI.

R GO; GC:0007050; P:cell cycle arrest; IDA.

R GO; GC:0005285; P:negative requlation of CDK activity; IDA.

R GO; GC:0008285; P:negative requlation of cell proliferation; IMP.

R Interpro; IPR003175; CDI.

R Pfan; PF0234; CDI:
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P27 kipl (Cyclin kinase inhibitor) (Cyclin dependent kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 197;
Pred. No. 21;
0; Mismatches 1; Indels
                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 AA.
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INTERACTION WITH NUPSO, AND MUTAGENESIS.
STRAIN=BALB/C;
MEDLINE=20271857; PubMed=10811608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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85.7%;
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SEQUENCE
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Matches
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                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-07-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 4 days neonate male adipose cDNA, RIEM full'length
enriched library, clone:B430307G09 product:cyclin-dependent kinase
inhibitor 1B (P27), full insert sequence (Mus musculus adult male
corpus striatum cDNA, RIKEN full-length enriched library,
clone:C030007E22 product:cyclin-dependent kinase inhibitor 1B (P27),
full insert sequence) (Mus musculus adult male liver tumor cDNA,
full-length enriched library, clone:C73002055 product:cyclin-
dependent kinase inhibitor 1B (P27), full insert sequence).
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STAIN=C57BL/6J; TISSUE-Adipose, Corpus striatum, and Liver;
STAIN=C9031; Pubmed=11076861;
A MEDLINE=203031; Pubmed=11076861;
A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Asiama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., A Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Toawa W., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Ookada K., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rokaki Y., Imusegrated sequence analysis (Rich S) system-384 format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STESUE-Adipose, Corpus striatum, and Liver; STRAIN=CSPEL/6J; TISSUE-Adipose, Corpus striatum, and Liver; Sdachi J., Alzawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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STRAIN=CS7BL/5G; TISSUE=Adipose, Corpus stria
MEDLINE=9927923; Pubwed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                  197 AA
                                                                                                      Created)
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Adipose, CC
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Adipose, C
MEDLINE=20499374; PubMed=11042159;
                                                                                                    (TrEMBLrel. 23,
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                Name=Cdkn1b;
                                                                                                    01-MAR-2003
                                                                  Q8BG74
                               RESULT 15
Q8BG74
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RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katch H., Kawai J., Kojina Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kutihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Satoch H., Saitoh H., Sakai C., Sakai K., Sakai W., Sano H.,
RA Sato R., Saltoh H., Sakai C., Sakai K., Sakaume N., Sano H.,
RA Tayawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tagami M.,
RA Tayawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tagami M.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
R. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
BR EMBL, AKO46676 BAC33119.1.
BR EMBL, AKO46676 BAC33119.1.
BR MGD, MGI.104565; Cdknlb.
BR GO, GO.000518; F.protein binding; IPI.
BR GO, GO.000518; F.protein binding; IPI.
BR GO, GO.0005059; F.protein binding; IPI.
BR GO, GO.0005059; P.negative regulation of cell proliferation; IMP.
BR GO, GO.000528; P.negative regulation of cell proliferation; IMP.
BR GO, GO.000528; P.negative regulation of cell proliferation; IMP.
BR GO, GO.000528; P.negative regulation of cell proliferation; IMP.
BR GO, GO.000528; P.negative regulation of cell proliferation; IMP.
BR GO, GO.000528; P.negative regulation of cell proliferation; IMP.
BR GO, GO.0005234; CDI:
BR FEMBL, PROSSES P. BR GO CO. S. SEQUENCE 197 As; 22193 NW; BAC300648B9BA3D6 CRC64;

Query Match
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Do LEGRYEW 76
Best Completed: October 26, 2004, 15:39:27
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October 26, 2004, 15:19:44; Search time 55.7692 Seconds (without alignments) 64.324 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* 4 6 9 7 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database :

	Description		Abg65743 Plant ICK	3738 Plant I	5737	5672 OSICF	5676 Broom	Abg65670 OsICK 2 p	5733 Plant	5739 Plant	Rice	Rice	Aap01953 Cyclin de	Soybe	Abg65673 Rice Os I	Rice	σ	Rice.		Soy	3321 St	085 Strept	5 Pl	3731 Plant	2677	1951 C	7253
SUMMARIES	ID		ABG65743	73	ABG65737	ABG65672		567	ABG65733	ABG65739	AAB26246	AAP01941	AAP01953	AAB27255	ABG65673	S		ABG65691	10	10	ABP28321	ABP30085	ABG65736	73		m	25
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AAB27257	AAY44339	AAE25107	AAY37054	AAB27259	AAY44340	AAE25108	AAW98180	AAE25111	ADN72351	ADB64165	AAM80167	AAB15554	AAM79183	AAM40879	AAW85727	AAU79304	ABU27245	AAU18386	AAY32132
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Inze D; Mironov V, Plant; inhibitor of cyclin dependent kinase; ICK. Droual A, Plant ICK protein conserved motif 1 #51. ABG65743 standard; peptide; 10 AA. Frankard VMS, Peres Bota AM, Hatzfeld Y; 29-JUN-2001; 2001WO-IB001492. 14-JUL-2000; 2000US-0218471P. 13-OCT-2000; 2000US-0241219P. (first entry) (CROP-) CROPDESIGN NV. WPI; 2002-471311/50. Sorghum bicolor. WO200228893-A2. 27-AUG-2002 11-APR-2002. ABG65743; RESULT 1 ABG65743

Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.

Disclosure; Page 14; 141pp; English.

This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to soreen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to ICK protein, forms which have decreased or aberrant activity compared to ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention

Matches

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RESULT 2 ABG65738

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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 5; Length 10;
Pred. No. 7.7;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; inhibitor of cyclin dependent kinase; ICK.
                                                                                                                    Plant; inhibitor of cyclin dependent kinase; ICK.
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                                                                                  Plant ICK protein conserved motif 1 #45.
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                                                                                                                                                                                                                                                               29-JUN-2001; 2001WO-IB001492.
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13-OCT-2000; 2000US-0241219P.
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                                                                                                                                                                                                                                                                                                                                                                                     Frankard VMS,
Hatzfeld Y,
                                                                                                                                                           Oryza sativa.
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                                                  27-AUG-2002
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               ABG65737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.
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Pred. No. 7.7;
0; Mismatches 5; Indels
                               Score 26; DB 5; Length 10;
Pred. No. 7.7;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mironov
                                                                                                                                                                                                                                                                                                                                                                        Plant; inhibitor of cyclin dependent kinase; ICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Droual A,
                                                                                                                                                                                                                                                                                                                                      Plant ICK protein conserved motif 1 #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 14; 141pp; English
                                                                                                                                                                                                                                 Ä.
                                                                                                                                                                                                                                 ABG65738 standard; peptide; 10
                              81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peres Bota AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-2000; 2000US-0218471P.
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50.0%;
                                                                     Conservative
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                                                                                                                                       EIEAFFAAAE
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Best Local Similarity
Matches 5; Conserv
                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa,
 Sequence 10
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11-APR-2002

ABG65737 standard; peptide; 10 AA.

RESULT 3 ABG65737

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Plant; inhibitor of cyclin dependent kinase; ICK.
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Hatzfeld Y;
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13-OCT-2000; 2000US-0241219P.
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                                                                                                                                                                                                                                        5; Conservative
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                                      (CROP-) CROPDESIGN NV
                                                   Peres
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N-PSDB; ABK93956.
                                                                      WPI; 2002-471311/50.
N-PSDB; ABK93952.
                                                                                                                                                                                                                                                                  67 EIEAFFAAAE
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                      treat disorders ch
of ICK inhibitors.
                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor.
                                                                                                                                                                                                              Sequence 87 AA;
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                                                   VMS,
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                                                  Frankard Hatzfeld
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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of substrates, drugs or compounds which modulate ICK activity, as well as to ICK protein, forms which have decreased or aberrant activity, as well as to ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
       Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
                                                                                                                                                                                                                                                                                                                                                                           81.2%; Score 26; DB 5; Length 108; 50.0%; Pred. No. 86;
                                                                                                    Claim 48; Example 5; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG65670 standard; protein; 262
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les 5; Conservative
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                                                                  of ICK inhibitors.
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Matches
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                                                                                                                                             Inze
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                                                                                                                                           Droual A, Mironov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                 Claim 48; Fig 4; 141pp; English.
                                                                                                                                             AM,
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50.0%;
                 29-JUN-2001, 2001WO-IB001492
                                                  14-JUL-2000; 2000US-0218471P
13-OCT-2000; 2000US-0241219P
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Gaps

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Indels

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Mismatches

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(first entry)

27-AUG-2002

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Gaps

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5; Indels

Mismatches

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Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
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Plant; inhibitor of cyclin dependent kinase; ICK.
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Hatzfeld Y;
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2000US-0241219F.
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N-PSDB; ABK93958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICK inhibitors.
                                                                                               WO200228893-A2
                                                  Oryza sativa.
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This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK

Claim 48; Fig 3; 141pp; English.

Inze

Mironov V,

Droual A,

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substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to the DNA and protein sequences of novel isolated the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of insufficient or excessive production of an ICK inhibitor. The protein of substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
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                                                                                                                                     Length 262;
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Pred. No. 2.1e+02;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mironov V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitor of cyclin dependent kinase; ICK.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Plant ICK protein conserved motif 1 #41.
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                                                                                                                                                                                                                                                                                                                  ABG65733 standard; peptide; 10 AA.
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                                                                                                                                   81.2%;
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                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                  217 EIEAFFAARE
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                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                   Sequence 262 AA;
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Hatzfeld Y;
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This invention relates to the DNA and protein sequences of novel isolated tack (Interpretation Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to sereen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or abstrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide user to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
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Pred. No. 13;
0; Mismatches
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                                                                                                                                                                                                                                                         Plant ICK protein conserved motif 1 #47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 14; 141pp; English.
                                                               10 AA
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13-OCT-2000; 2000US-0241219P.
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50.0%;
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                                                         ABG65739 standard; peptide;
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les 5; Conservative
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                                                                                                                         ABG65739;
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ABG65739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequence is the rice CDKI clone rsr9n.pk003.g12 as described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
                                     Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0117.h4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.1%; Score 25; DB 3; Length 46; 50.0%; Pred. No. 63; 21ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Е.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP01953 standard; protein; 60 AA.
                                                                                                     Claim 10; Page 40; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN02403
N-PSDB; AAN02391
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060087-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin dependent kinase inhibitor, CDKI, herbicide, cell cycle, rice, plant growth inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice Cyclin dependent kinase inhibitor (CDKI) clone rsr9n.pk003.g12.
                                                                                                                                                                                                                                                                                                                                                                                             Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 40; 58pp; English.
                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                          Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weng Z, Cahoon RE;
                                                                                                                                                              06-APR-2000; 2000WO-US009106.
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50.0%;
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es 5; Conservative
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cell growth; herbicide.
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                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679375/66
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                                                                                                                                                                                                                                                                                          Weng Z,
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA95277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200060087-A2
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                                       Oryza sativa.
                                                                                                                                                                                                        07-APR-1999;
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                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                                                                          Klein TM,
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AAP01941;

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RESULT 10 AAP01941

Query Match

Matches

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RESULT 13
ABG65673
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acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the soybean CDKI clone $12.pk0117.h4 as described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the soybean cyclin-dependent kinase inhibitor (CDKI). Its coding sequence was isolated by searching a soybean seedling cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in
                                                                                                                                                                                                                                                                                                                                                  Soybean, cyclin-dependent kinase inhibitor; cell cycle, cell division, CDKI; cell growth, herbicide.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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                                                                                                                      Score 25; DB 3; Length 60;
Pred. No. 82;
                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                            Soybean cyclin-dependent kinase inhibitor #4.
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Pred. No. 82;
0; Mismatches
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                                                                                                                       78.1%;
50.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                     1 EXEXFFXXXE 10
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N-PSDB; AAA95289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other organisms
                                                                                                Sequence 60 AA;
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Mironov V,

Droual A,

Peres Bota AM,

Frankard VMS,

Hatzfeld

Plant; inhibitor of cyclin dependent kinase; ICK

29-JUN-2001; 2001WO-IB001492.

WO200228893-A2.

11-APR-2002

Oryza sativa.

14-JUL-2000; 2000US-0218471P. 13-OCT-2000; 2000US-0241219P.

(CROP-) CROPDESIGN NV

Rice Os ICK associated peptide.

27-AUG-2002

ABG65673;

ABG65673 standard; protein; 90 AA.

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                                                                                                                                                                                         This invention relates to the DNA and protein sequences of novel isolated ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of insufficient or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity, as well as to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                       Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice; cyclin-dependent kinase inhibitor; CDXI; cell cycle; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.20+02;
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                                                                                                                                                        Claim 48; Disclosure; 141pp; English.
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50.0%;
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WPI; 2002-471311/50.
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Best Local Similarity
                                                                                                            ICK inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90
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Matches
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Length 60;

DB 3;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclin dependent kinase inhibitor; CPKI; herbicide; cell cycle; rice; plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                     Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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                                                                                                                                                                           Weng Z, Cahoon RE;
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                                                                                                06-APR-2000; 2000WO-US009106.
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Best Local Similarity 50.0%;
Matches 5; Conservative
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cell growth; herbicide
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N-PSDB; AAA95285.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99 AA;
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                          Oryza sativa.
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                                                                          12-OCT-2000.
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WPI; 2000-679375/66

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                                                                                                                                The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic act sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used so harbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the rice CDKI clone rar9n.pk003.g12.fis as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                 Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 3; Length 99;
Pred. No. 1.4e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: October 26, 2004, 15:36:54 Job time : 57.7692 secs
                                                                                                      Claim 10; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
For S, Conservative
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N-PSDB; AAN02399
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Run on:

Title:

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Sequence 4, Application US/09526597D
; Sequence 4, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFREENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
                           Sequence 4, Appli
Sequence 24, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 1488, Appli
Sequence 2488, Appli
Sequence 4465, Appli
Sequence 4845, Appli
Sequence 6434, Appli
Sequence 6863, Appli
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              Sequence
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Pred. No. 1.7e+02;
0; Mismatches 5; Indels
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Patent No. 6358738

GENERAL INFORMATION:
APPLICANT: Erikson, et al.
TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
TITLE OF INVENTION: METHODS, AND USES THEREFOR
FILE REFERENCE: 1874/110.
CURRENT APPLICATION NUMBER: US/09/311,311C
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,296
PRIOR PRIARE PRESENCE: 1998-05-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PRESENCE: 1988-06-13
LENGTH SASTERE PRESENCE FOR WINDOWS VERSION 4.0
SEQ ID NO 24
LENGTH: S83
US-09-177-650-89
US-09-819-148-4
US-09-950-304-4
US-09-105-058C-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-177-650-2
US-09-178-1010-4465
US-09-134-001C-4940
US-09-134-001C-4940
US-09-134-011C-4940
US-09-134-011C-4940
US-09-134-011C-4940
US-09-178-1863
US-09-176-1828-5863
US-09-176-761328-5863
US-09-176-761328-5863
US-09-177-767-61925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.0%;
Best Local Similarity 50.0%;
Matches 5; Conservative
     181 ÉMÉRFFAYAÉ 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mus musculus
     FEATURE:
NAME/KEY: CHAIN
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US-09-311-311C-24
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Sequence 54, Appl
Sequence 6482, Appl
Sequence 5761, Ap
Sequence 1540, Ap
Sequence 154, Appl
Sequence 157, Appl
Sequence 25757, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 25757, Appl
Sequence 25757, Appli
Sequence 3, Appli
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9, Appli
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                                                                                                   October 26, 2004, 15:19:44 ; Search time 16.5385 Seconds (without alignments) 40.099 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Sequence 1
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                                                                                                                                                                                                                                                                                   478139
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/cgn2 6/ptodata1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata1/liaa/5B_COMB.pep:*
/cgn2 6/ptodata1/liaa/6A_COMB.pep:*
/cgn2 6/ptodata1/liaa/6B_COMB.pep:*
/cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*
/cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*
/cgn2 6/ptodata1/liaa/backfiles1.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-526-597D-4
US-09-311.311C-24
US-09-311.311C-24
US-09-134-000C-5761
US-09-134-000C-6140
US-09-26-597D-2
US-09-291-417D-154
US-09-688-1888-154
US-09-688-1888-154
US-09-688-1888-155
US-09-688-1888-155
US-09-688-1888-155
US-09-291-417D-155
US-09-291-417D-155
US-09-291-417D-155
US-09-198-452A-1014
US-09-198-452A-1014
US-09-198-452A-1014
US-09-198-452A-1014
US-09-291-317D-33
US-09-291-317D-33
US-09-388-335-3
US-09-388-335-3
US-09-297-977C-9
US-09-297-977C-9
US-09-297-977C-9
US-09-297-977C-9
US-09-297-977C-9
US-09-297-977C-9
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
                                                                                                                                                          US-09-574-735C-36
32
1 EXEXFFXXXE 10
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Maximum DB 8
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Result

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Sequence 6140, Application US/09134000C

Sequence 6140, Application US/09134000C

Patent No. 6417156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BWTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BWTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-002

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR PAPLICATION NUMBER: US 60/055,778

PRIOR PAPLICATION STATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

LENGTH: 117
                                                                                                                            GENERAL INFORMATION:
APPLICANT: LYND DOUGCHEE-Stamm et al
APPLICANT: LYND DOUGCHEE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 02796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRICR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PARENTIN Version 3.1
SEQ ID NO 5761
LENGTH: 117
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APPLICANT: De Veylder, Lieven
APPLICANT: De Almeida, Janice
APPLICANT: Landrieu, Isabelle
TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
FILE REFERENCE: 1187-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 4; Length 117;
Pred. No. 1.5e+02;
0; Mismatches 5; Indels
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Pred: No. 1.5e+02,
0, Mismatches 5, Indels
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                                                                   Sequence 5761, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09526597D Patent No. 6710227
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ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
, ORGANISM: Enterococcus faecalis
US-09-134-000C-6140
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50.0%;
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50.08;
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Best Local Similarity 50.v.
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US-09-526-597D-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                               Score 24; DB 3; Length 583; Pred. No. 4.4e+02; 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPANING SYSTEM: «Unknown»
COFTWARE: ASCII
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/055,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1017, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ARITICALION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION INFORMATION:
TELECOMMUTICATION INFORMATION:
AMMERIANING THE AND TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...117

; SEQUENCE DESCRIPTION: SEQ ID NO: 6482:

US-09-107-532A-6482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6482, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
; LOCATION: (1)...(583)
; OTHER INFORMATION: GRASP65 protein US-09-311-311C-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6482:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                               75.0%;
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                          Best Local Similarity 50.0
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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US-09-107-532A-6482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 4; Length 966; Pred. No. 1.2e+03; 0; Mismatches 5; Indels
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JOS-09-08-1-205-1-107.

JOS-09-08-1-205-1-107.

JOS-08-1-205-1-107.

JOS-08-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108-1-108
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US-09-291-417D-154

VS-09-291-417D-154

Sequence 1154, Application US/09291417D

Patent No. 6680170

GENERAL INFORMATION:

APPLICANT: PLOWAN, GREGORY

APPLICANT: MARTHE, DAVID

TILLE OF INVENTION: STE20-RELATED PROTEIN KINASES

TILLE OF INVENTION: STE20-RELATED PROTEIN KINASES

CURRENT APPLICATION NUMBER: US/09/291, 417D

CURRENT FILING DATE: 1999-04-13

PRIOR FILING DATE: 1998-04-14
   Mismatches
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50.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
LENGTH: 966
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
      5; Conservative
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                                                                                                                     933 EQEMPFKLSE 942
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CORGANISM: Homo sapiens
US-09-688-1888-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Murine sp.
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US-09-688-188B-155
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US-09-688-188B-107
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         Matches
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i Sequence 18565, Application US/09248796A

patent No. 6747137

GENERAL INFORMATION:

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PLING DATE: 1998-02-13

PRIOR PLING DATE: 1998-02-13

PRIOR PLING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18585

LENGTH: 860

LENGTH: 860
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.7e+02;
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US-09-688-188B-154
| US-09-688-188B-154
| Sequence 154, Application US/09688188B
| Patent No. 6656746
| GENERAL INPORMATION:
| APPLICANT: MARTINEZ, RICARDO
| APPLICANT: MARTINEZ, RICARDO
| APPLICANT: MARTINEZ, RICARDO
| TITLE OF INVENTION: STE2O-RELATED FROTEIN KINASES
| PILE REFERENCE: 038602/0328
| CURRENT APPLICATION NUMBER: 09/09/1417
| PRIOR FILING DATE: 1999-04-14
| PRIOR FILING DATE: 1999-04-14
| NUMBER OF SEQ ID NOS: 155
| SEQ ID NO 154
                                                                                                                                                                                                              Query Match 71.9%; Score 23; DB 4; Best Local Similarity 50.0%; Pred. No. 2.7e+02 Matches 5; Conservative 0; Mismatches
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50.0%;
                                                                                                  TYPE: PRT ORGANISM: Arabidopsis thaliana
               SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-18585
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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ORGANISM: Murine sp.
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                                           SEQ ID NO 2
LENGTH: 209
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0; Mismatches
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PRIOR APPLICATION NUMBER: 60/081,784
PRIOR PILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver: 2.1
FEMALE: PATENTIN VER: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Chlamydia pneumoniae US-09-198-452A-1014
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50.0%;
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66.7%;
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Similarity 66.7%;
4; Conservative
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; ORGANISM: Proteus mirabilis
US-09-543-681A-7484
                                                                                                                                                                                                                              Query Match 71.9
Best Local Similarity 50.0
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7,
...ches 4; Conservative
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                                                                                                                              LENGTH: 968
TYPE: PRT
CRGANISM: Homo sapiens
US-09-291-417D-155
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Best Local Similarity
Matches 4; Conserv
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US-09-543-681A-7484
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US-09-198-452A-1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 4; Length 968
Pred. No. 1.2e+03;
0; Mismatches 5; Indels
  Sequence 155, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWMAN, CREGORY
APPLICANT: PLOWMAN, CREGORY
APPLICANT: MATTINEZ, RICARDO
APPLICANT: WHYTE, DAVUD
TITLE OF INVENTYON: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: 09/294,417
PRIOR PILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PALENT Ver. 2.1
SSOFTWARE: PALENT Ver. 2.1
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Patent No. 6680170
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARO
APPLICANT: MARTINEZ, RICARO
APPLICANT: MARTINEZ, RICARO
TILLE OF INVENTION: STE2O-RELATED PROTEIN KINASES;
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-14
NUMBER OF SEC ID NOS: 155
SECTIORNO 107
LENGTH: 968
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US-09-291-417D-155
Sequence 155, Application US/09291417D
Sequence No. 6680170
GENERAL INFORMATION:
APPLICANT: PLOWAN, GREGORY
APPLICANT: MARYINEZ, RICARDO
APPLICANT: MARYINEZ, RICARDO
APPLICANT: MARYINEZ, RICARDO
FILE OF INVANION: $7E20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
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Best Local Similarity 50.0%;
Matches 5; Conservative (
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US-09-688-188B-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-09-291-417D-107
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Best Local Similarity
'-hea 5; Conserve
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US-09-291-417D-107
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Sequence 1014, Application US/09198452A.
Patent No. 6559294
GABERLI INFORMATION:
APPLICANT: GTIffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REPERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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GENERAL INC. 802709

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US/09/543,681A

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7484

LENGTH: 248
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Pred. No. 4.6e+02;
0; Mismatches 2; Indels
  Length 968;
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Pred. No. 5.5e+02;
0; Mismatches 2; Indels
                                                 5; Indels
Score 23; DB 4; 1
Pred. No. 1.2e+03;
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Wed Oct 27 09:35:40 2004

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Search completed: October 26, 2004, 15:34:20 Job time : 17.5385 secs

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October 26, 2004, 15:19:44 ; Search time 143.846 Seconds (without alignments) 22.507 Million cell updates/sec
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| cgn2 \( \frac{6}{\} \text{prodata} 2 \) \text{pubpa} \( \text{VBCOMB} \). \text{PUB \( \t
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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32
1 EXEXFFXXXE 10
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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!	Appl	Appl	198574,	10, Appl	195115,	13, Appl	263, 7	44, Appl	120870,	2928,	128205,	59718, 7	61054, 7
<u> </u>	12,	16,					36						
Description	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence
Sa	US-10-333-006-12	-006-16	-963-198574	US-10-333-006-10	US-10-437-963-195115	US-10-333-006-13	-701-36263	-006-44	-963-120870	-599-182928	US-10-437-963-128205	JS-10-425-114-59718	JS-10-425-114-61054
SUMMARIES	-333	-333	-437	-333	-437	-333	-767	-333	-437	-424	-437	-425	-425
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DB	15	15	19	H	16	H	7	-	7	7	16	H	H
Length DB	87	108	225	262	417	90	95	194	194	205	218	248	255
% Query Match	81.2	81.2	81.2	81.2	81,2	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1
Score	26	26	26	26	26	25	25	25	25	25	25	25	25
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0-369-493-2272	.0-369-493-	.0-369-493-2280	0-333-006-1	.0-767-701-5	US-09-733-507-14	US-10-451-139-1	us-	US-09-733-507-16	US-10-451-139-15	US-10-424-599-2	US-10-688-291	US-10-451-139-21	US-10-104-047	US-10-013-477-14	US-10-437-963-17778	US-10-437-963-17778	US-10-282-122A-5516	US-10-369-493-622	US-10-156-761-963	US-10-114-893-12	880-192-	-427-348-	54-408A-	3-507-11	US-10-451-139-	3-507-2	3-507-1	US-10-451-139	US-10-688-291-2	US-10-451-139-19	US-10-156-761-9
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ALIGNMENTS

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US-10-334-006-12, Agplication US/10333006

SEQUENCE 12, Application No. US20040019926All

GENERAL INFORMATION:

APPLICANT: Frankard, Valerie Marie-No. US20040019926Allle S.

APPLICANT: Process Bota, Adrian Marius

APPLICANT: Misser Bota, Adrian Marius

APPLICANT: Misser Bota, Valadimir

APPLICANT: Misser Bota, Valadimir

APPLICANT: Misser Inso, Dirk

APPLICANT: Hatzfeld, Yves

FILE REFRENCE: 1187-13

CURRENT FILING DATE: 2003-01-14

PRIOR FILING DATE: 2003-01-14

PRIOR FILING DATE: 2001-01-14

PRIOR FILING DATE: 2000-07-14

NUMBER OF SEQ ID NOS: 5-9

SOFTWARE: PART

ORGANISM: Oryza sativa

US-10-333-006-12

Query Match

Best Local Similarity 50.0%; Pred. No. 99;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps
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67 EIEAFFAAAE

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173 EIEAFFAAE 182

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APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad Till Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21 (53221) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                         APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S. APPLICANT: Feres Bota, Adrian Marius APPLICANT: Peres Bota, Adrian Marius APPLICANT: Peres Bota, Adrian Marius APPLICANT: Drough, Anne-Marie APPLICANT: Mironov, Vladimir APPLICANT: Inz, Dirk APPLICANT: Harzfeld, Yves TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS FILE REFERENCE: 1187-13
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Pred. No. 2.9e+02;
0; Mismatches 5; Indels
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US-10-437-963-195115
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CURRENT APPLICATION NUMBER: US/10/333,006

CURRENT FILING DATE: 2003-01-14

PRIOR APPLICATION NUMBER: US CUT/1B01/01492

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2000-07-14

PRIOR PLICATION NUMBER: US 60/218,471

PRIOR PLICATION NUMBER: US 60/218,471

PRIOR PLICATION NUMBER: US 60/241,219

PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 262

TYPE: PATENT SEQ ID NOS: 59

CENTRY: 263

SOFTWARE: PATENT NOS: 59

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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: AR ROSa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 195115
LENGTH: 417
                                                     Sequence 10, Application US/10333006
Publication No. US20040019926A1
GENERAL INFORMATION:
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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ORGANISM: Oryza sativa
FEATURE:
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US-10-437-963-195115
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Sequence 198574, Application US/10437,963

SEQ ID NOS: 204966

SEQ ID NOS: 204966

SEQ ID NOS: 204966

SEQ ID NOS: 204966

SEQ ID NOS: 204966
Sequence 16, Application US/10333006
Sequence 16, Application US/10333006
Sequence 16, Application US/10333006
Sequence 16, Application No. US20040019926All
SPELICANT: Frankard, Valerie Marie-No. US20040019926Allle S. APPLICANT: Proual, Anne-Marie
APPLICANT: Mironov, Vladimir
APPLICANT: Mironov, Vladimir
APPLICANT: Hazzeld, Yvee
ITLE OF INVENTION: UNMER: US/10/333,006
CURRENT APPLICATION NOWEE FLANT CYCLIN-DEPENDENT KINASE INHIBITORS
FILE REFERENCE: 1187-13
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: DG 60/218,471
PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
SPRIOR PELING DATE: 2000-07-14
SPRIOR PELING DATE: 2000-07-14
SPRIOR PELING DATE: 2000-07-14
SPRIOR PELING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Petentin version 3.1
SEQ ID NO 16
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Pred. No. 1.2e+02;
0; Mismatches 5; Indels
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US-10-437-963-198574
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Best Local Similarity 50.0%;
Matches 5; Conservative
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ORGANISM: Sorghum bicolor
US-10-333-006-16
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Best Local Similarity 50.0
Matches 5; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-198574
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APPLICANT: A Road Inches J.
APPLICANT: E Road Inches J.
APPLICANT: E Road Inches J.
APPLICANT: Coo, Yongwel
APPLICANT: Coo, Yongwel
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBICE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120870
Sequence 44, Application US/10333006

Sequence 44, Application US/10333006

Publication No. US20040019926A1

GENERAL INFORMATION:

APPLICANT: Peres Bota, Adrian Marius
APPLICANT: Droual, Anne-Marie
APPLICANT: Inz, Dirk
APPLICANT: Mironov, Vladimir
APPLICANT: Marzfeld, Yves
Inz, Dirk
APPLICANT: Harzfeld, Yves
Inz, Dirk
APPLICANT: Harzfeld, Vves
FILE REFERENCE: 1187-13
CURRENT APPLICATION NUMBER: US/10/333,006
CURRENT APPLICATION NUMBER: US/10/333,006
CURRENT APPLICATION NUMBER: US/00/1-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-4
PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR APPLICATION NUMBER: US 60/214,219
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
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US-10-437-963-120870
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Pred. No. 3.7e+02;
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Best Local Similarity 50.0
Matches 5; Conservative
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Matches 5; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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Sequence 16263, Application Wo. US20040172684A1

Publication No. US20040172684A1

REBERRATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 19-238-21 US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 36263

LENGTH: 95
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                                                                                                                                                                              GREERAL INFORMATION:
APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.
APPLICANT: Frankard, Valerie Marius
APPLICANT: Froual, Anne-Marie
APPLICANT: Droual, Anne-Marie
APPLICANT: Droual, Anne-Marie
APPLICANT: Hazield, Yves
III, Dirk
APPLICANT: Hazield, Yves
IIIE REFERENCE: 1187-13
FILE REFERENCE: 1187-13
FILE REFERENCE: 1187-13
FILE REFERENCE: 1001-06-29
FRIOR PAPLICATION NUMBER: DCT/IBO1/01492
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
SPRIOR FILING DATE: 2000-07-14
SPRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 59
SOFTWARKE: Patentin Version 3.1
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 15; Length 90;
Pred. No. 1.7e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C86129_1.pep
US-10-767-701-36263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                  Sequence 13, Application US/10333006 Publication No. US20040019926A1 GENERAL INFORMATION:
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ilarity 50.0%;
Conservative
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Best Local Similarity 50.0%;
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXEXFFXXXE 10
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    372 ÉIÉAFFAAAE 381
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US-10-333-006-13
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Best Local Similarity
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US-10-767-701-36263
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US-10-425-114-61054

US-10-425-114-61054

Sequence 61054, Application US/10425114

Publication No US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Pabaska, Jack E
APPLICANT: Pabaska, Usok E
APPLICANT: Pabaska, Usok E
APPLICANT: Pabaska, Usok E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)
CURRENT PILING DATE: 2003-04-28

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 61054

LENGTH: 255

LENGTH: 255
                                                     GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Screen, Jock E
APPLICANT: Passks, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59118
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: LIB3732-047-G6_FLI.pep
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US-10-425-114-61054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.1%; Score 25; DB 15;
50.0%; Pred. No. 4.7e+02;
iive 0; Mismatches 5
Sequence 59718, Application US/10425114
Publication No. US20040034888A1
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Best Local Similarity 50.0
Matches 5, Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-114-59718
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US-10-369-493-22727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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| Publication No. US2004012334341
| Publication No. US2004012334341
| Publication No. US2004012334341
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: Cao, Yohua |
| APPLICANT: Cao, Yohua |
| APPLICANT: Cao, Yohua |
| APPLICANT: Www with weight of the proposed 
Sequence 182928, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANT: 2003-04-28
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pep
US-10-424-599-182928
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US-10-437-963-128205
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
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RESULT 15

US-10-369-493-22728

J Sequence 22728

J Sequence 22728

J Sequence 22728

J Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Geo, Yongwel

J APPLICANT: Goldman, Marry S.

APPLICANT: Goldman, WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 30-10 (520.52) B.

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

FRIOR FILING DATE: 2002-02-21

SEQ ID NO 22728

LENGTH: 401
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ENANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FURRENT APPLICATION NUMBER: US10/369,493
CURRENT FILING DATE: 2002-02-8
PRIOR FILING DATE: 2002-02-8
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22727
LENGTH: 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(401)

COTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-22727
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ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
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Search completed: October 26, 2004, 15:33:30 Job time : 144.846 secs

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1 EXEXPEXXXE 10

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October 26, 2004, 15:27:13 ; Search time 13:8462 Seconds (without alignments) 69.490 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           283416 seqs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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32
1 EXEXFFXXXE 10
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                        Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypother	septin homolog - f	probable salt-indu	cyclin-dependent k	hypothetical prote	stage V sporulatio	DNA ligase TC0423	probable DNA ligas	hypothetical prote	phospholipase D (E	hypothetical prote	YUP8H12.5 [importe	nucleoside-diphosp	probable flavodoxi	othe	hypothetical prote	ᇃ.	٠,	-			hypothetical prote	phosphoenolpyruvat	neuronal cell cycl	ത	complement compone	nucleoside diphosp	hetica	sipe protein - sai
SUMMARIES	σī	B71318	862523	T02656	T09968	T15928	C83945	A81704	C71551	T26811	T04092	B81014	B86188	C97710	F71263	A69950	T42687	T01132	AE1632	T46140	876519	T20748	T31064	F75415	A56677	T22493	I50806	C82283	AB0851	870217
	DB	N	N	N	N	N	7	7	N	7	0	Ŋ	N	Ŋ	N	(7	N	7	Ŋ	N	N	N	N	(1	N	~	0	0	7	7
	Length	62	380	799	196	299	315	660	663	786	808	79	137	140	146	146	155	191	200	209	355	364	474	829	1251	1425	1673	142	165	165
d€	ery	78.1	78.1	78.1	75.0	75.0	75.0	75.0	75.0	75.0	75.0	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	68.89	68.8	68.8
	Score	25	25	25	24	24	24	24	24	24	24	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	22	22	22
,	Result No.		7	ო	4	ιΩ	ω	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

sicA protein - Sal	hypothetical prote	chromosome partiti	hypothetical prote	hypothetical prote	conserved hypothet	extragenic suppres	extragenic suppres	conserved hypothet	calretinin - chick	calretinin - human	calretinin - rat	p37NB - human	UDP-N-acetylglucos	two component sens	nitrogen regulatio
A57357	H96532	н69060	C75552	T33829	AB0832	AB1208	AE1564	E69455	A27067	A60253	825006	G02020	E83970	AE2754	C97535
N	~	7	(1	N	N	~	~	N	,	Н	н	N	N	(7)	(7)
165	195	218	230	233	243	257	257	261	269	271	271	313	363	382	382
68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	8	8.89	68.8
22	22	22	22	22	22	22	22	22	22	22	22	0	0	2 2	22

ALIGNMENTS

,	RESULT 1 B71318 C.Goraerved hypothetical protein TP0490 - syphilis spirochete C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C.Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C.Dates: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C.Dates: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwirson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD science 281, 375-388, 1998 A,Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. S.A.Reference number: A71250; MuID:98332770; PMID:965876 A,Reference number: A71250; MuID:98332770; PMID:965876 A,Scatus: proliminary; nucleic acid sequence not shown; translation not shown A,Residues: 1-62 cCOL> A,Cross_references: UNIPRCT:083503; GB:AE001225; GB:AE000520; NID:g3322775; PIDN:AAC654 A;Gene: TP0490
	Query Match 78.1%; Score 25; DB 2; Length 62; Best Local Similarity 50.0%; Pred. No. 9.8; Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy 1 EXEXPEXXXE 10 Db 52 EAEDFFGSAE 61
	RESULT 2 S62523 septin homolog - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 16-May-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004 C;Date: 16-May-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: T41191; T41431; T39129; S65523 R;Lyre, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D. Submitted to the EMBL Data Library, April 1999 A;Reference number: Z21976 A;Accession: T41191 A;Status; preliminary; translated from GB/EMBL/DDBJ
	A;Molecule type: DNA A;Residues: 1-380 (LINA) A;Cross-references: UNIPROT:Q09883; EMBL:AL049662; PIDN:CAB41232.1; GSPDB:GN00068; SPDB A;Cross-references: UNIPROT:Q09883; EMBL:AL049662; PIDN:CAB41232.1; GSPDB:GN00068; SPDB A;Cross-references: strain 972h-; cosmid C188 A;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1998 A;Reference number: Z21993 A;Reference number: Z21993 A;Accession: T41431 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-380 <see></see>

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C'Species: Chenopodium rubrum (red goosefoot)
C'Species: La-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C'Accession: T09968
R'Fountain, M.D.; Renz, A.; Beck, E.
R'Fountain, M.D.; Renz, A.; Beck, E.
A;Fountain, M.D.; Renz, A.; Beck, E.
A;Accession: T09968
A;Accession: T09968
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A;Molecule type: DNA
A;Residues: 1-29 cCHI.
A;Cross-references: UNIPROT: 009529; EMBL: UZ3484; NID: g733597; PID: g733599; PIDN: AAC46762
A;Experimental source: strain Bristol N2
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Nucleic Acids Res. 28, 4317-4331, 2000
Affile: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stage V sporulation protein K BH2363 [imported] - Bacillus halodurans (strain C,Species: Bacillus halodurans C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Type: mRNA
A;Molecule : 1-196 (*POU>
A;Residues: 1-196 (*POU>
A;Residues: 1-196 (*POU>
A;Cross-references: UNIPROT:048597; EMBL:AJ002173
A;Experimental source: photoautotrophic cells derived from hypocotyl tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein EEED8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15928
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                                                                                                       red goosefoot
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Pred. No. 91;
0; Mismatches
                                                                                                          protein
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                                                                                                       cyclin-dependent kinase inhibitor
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Best Local Similarity 50.0
Matches 5, Conservative
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A;Introns: 84/3; 133/3; 275/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164
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les 5; Conserv
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C83945
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NiAlternate names: hypochetical protein F12C20.17
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Nar-1999 #sequence_revision 24-Nar-1999 #text_change 09-Jul-2004
C;Date: 24-Nar-1999 #sequence_revision 24-Nar-1999 #text_change 09-Jul-2004
R;Rounsley, S.D; Roming, C.M.; Lin, X; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy
submitted to the EMBL Data Library, August 1999
A;Posestription: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.
A;Reference number: 21688
A;Residus: 1-799 KRDJ.
A;Reference number: 21688
A;Residus: 1-799 KRDJ.
A;Residus: 1-799 KRDJ.
A;Cross-reference: UNIPRO7:081028; EMBL.AC005168; NID:g3426033; PID:g3426046
A;Residus: 1-799 KRDJ.
A;Cross-reference: UNIPRO7:081028; EMBL.AC05168; NID:g3426033; PID:g3426046
A;Residus: 1-799 KRDJ.
A;Cross-reference: UNIPRO7:081028; EMBL.AC05168; NID:gate033; PID:gate046
A;Cross-reference: UNIPRO7:081028; EMBL.AC05168; NID:gate047, S.L.; Fraser, C.M.; Venter, J.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Tile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Residues: 1-799
C;Geneile type: DNA
A;Residues: 1-799
C;Geneile type: DNA
A;Residues: 1-799
C;Geneile: Signos
A;Gene: F12C20.17; At2g26790
                                                                                                             A;Reference number: Z21830
A;Accession: T39129
A;Status: Perliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-380 <LY2>
A;Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91517.1; PID:g1052538; SPDB:SPACE
A;Cross-references: EMBL:AL032824; PIDN:CAB37422.1; GSPDB:GN00068; SPDB:SPCC584.09
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0
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A;Introns: 20/2
C;Superfamily: Saccharomyces cerevisiae cell division control protein CDC10
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                               A; Experimental source: strain 972h-; cosmid c584
R; Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, November 1995
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Pred. No. 1.4e+02;
0; Mismatches 5; Indels
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Pred. No. 65;
0; Mismatches
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Best Local Similarity 50.0%;
Matches 5; Conservative
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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C,Genetics: <LY23>
A,Gene: SPDB:SPAC8A4.07
                                                                                                                                                                                                                                                                                            C,Genetics: <LYN1>
A,Gene: SPCC188.12
A,Map position: 3
A;Introns: 20/2
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A;Gene: SPCC584.09
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Gaps

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C-125)

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-315 <STO>

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Gaps

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A;Residues: 1-786 <WIL>
A;Cross-references: UNIPROT:062431; EMBL:Z95559; PIDN:CAB08998.1; GSPDB:GN00022; CESP:Y·
A;Experimental source: clone Y41E3
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phospholipase D (EC 3.1.4.4) - common tobacco)
(Species: Nicotiana tabacum (common tabacum)
(Species: Nicotiana tabacum)
(Species: Characterization of tobacco phospholipase D.
(Species: Total taracterization of tobacco phospholipase D.
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By 10-1
By 1
                                                                                                                                    hypothetical protein Y41E3.4 - Caenorhabditis elegans Cippedies: Caenorhabditis elegans Cippedies: Caenorhabditis elegans Cipate: 15-Oct-1999 #text_change 09-Jul-2004 Cipate: 15-Oct-1999 #text_change 09-Jul-2004 Cipate: 15-Oct-1999 #text_change 09-Jul-2004 Cipate: 15-Oct-1999 #text_change 09-Jul-2004 Rivenurray, A.

Rivenurray, A.

A;Reference number: 220270
A;Reference number: 220270
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Introns: 83/3; 195/3; 357/3; 573/2; 749/2
C,Superfamily: human glutamine-tRNA ligase; glutamine-tRNA ligase homology
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Pred. No. 2.6e+02; 
0; Mismatches 5; Indels
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Pest Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels
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Best Local Similarity 50.0
Matches 5; Conservative
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A;Gene: CESP:Y41E3.4
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C;Species: Chlamydia trachomatis
C;Stace 13.58p-1998 #sequence_revision 13.58p-1998 #text_change 12-Jul-2004
C;Accession: C71551
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-799, 1998
A;Accession: C71551
A;Accession: C71551
A;Accession: C71551
A;Accession: C71551
A;Accession: C71551
A;Accession: C71551
A;Residues: 1-663 <ARN>
A;Cross-references: UNIPROT:084148; GB:AE001288; GB:AE001273; NID:g3328545; PIDN:AAC6773
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Chlamydia muridarum, Chlamydia trachomatis Nopn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 12-Jul-2004
C;Accession: A81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUD:20150255; PMID:10684935
A;Accession: A81704
A;Accession: A81704
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-660 cTET>
A;Residues: 1-660 cTET>
A;Residues: UNITROT:Q9PKP2; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3927
GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06d
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Pred. No. 2.1e+02;
0; Mismatches 5; Indels
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Pred. No. 2.1e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                        Length 315;
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Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
A;Cross-references: UNIPROT:09KAC6;
A;Experimental source: strain C-125
C;Genetics:
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ilarity 50.0%;
Conservative (
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Best Local Similarity 50.0%;
Matches 5; Conservative
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C;Superfamily: cfxQ protein
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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A;Gene: TC0423
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Conserved hypothetical protein yqcK - Bacillus subtilis
C;Species: Bacero, N.; Moszer, I.; Albertini, R.M.; Alloni, G; Azevedo, V.; Berter
C;Species: Species: Bacero, B.T. Fritz, C; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
S; Ayuthors: Foulger, D.; Fritz, C; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
S; Koetter, P.; Koningstein, G; Krogh, S.; Kumano, M.; Kurita, R.; Lapidus, A.; Laulio, M.F.
Koetter, P.; Koningstein, G.; Rocha, B.; Rark, S.H.; Parro, V.; Pohl, T.M.; Parrot, V.; Garaneol, S.; Maueel
Y, M.; Ogdwa, K.; Ogiwara, A.; Odudega, B.; Rose, M.; Sakiguchi, J.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Yamanoto, H.; Yamanoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Alticle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:9849377
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Skesidues: 1-146 cCOL-
A;Cross-references: UNIRROT:083895; GB:AE001261; GB:AE000520; NID:g3323243; PIDN:AAC6588-
A;Experimental source: strain Nichols
                                            A,Molecule type: DNA
A,Residues: 1-140 «KUR»
A,Cross-references: UNIPROT:092J14; GB:AE006914; PIDN:AAL02621.1; PID:g15619121; GSPDB:©
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Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876 A;Accession: F71263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable flavodoxin - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: F71263
                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 2; Length 140;
Pred. No. 74;
0; Mismatches 5; Indels
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C;Keywords: electron transfer; flavoprotein; FMN
F;6-145/Domain: flavodoxin homology <FLX>
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77;
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C,Superfamily: Nucleoside diphosphate kinase
C,Keywords: phosphotransferase
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Pred. No. 7
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50.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative (
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Best Local Similarity 50.0
Matches 5; Conservative
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A;Status: preliminary
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                                                                                                             A/Fesiques: 1-/9 clairs
A/Fittle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A/Accession: F81956
A/Accession: F81956
A/Accession: F81956
A/Fesiques: 1-/9 cPAR>
A/
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A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Soley, T.; Rowley, D.; Sakano, H.
A, Althors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A, Mittle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A, Reference number: A86141; MUID:21016719; PMID:11130712
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797710
1026-0816-diphosphate kinase (EC 2.7.4.6) [imported] - Rickettsia conorii (strain Malis nucleoside-diphosphate kinase (EC 2.7.4.6) [imported] - Rickettsia conorii (strain Malis C; Species: Rickettsia conorii
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
R; Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc Science 293, 2093-2098, 2001
A; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A; Reference number: A97700; MUID:21442074; PMID:11557893
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A,Residues: 1-137 <STO>
A,Cross-references: UNIPROT:023036; GB:AE005172; NID:g2388563; PIDN:AAB71444.1; GSPDB:GN
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86188
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel. N.A. Kaul S. white
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Pred. No. 72;
0; Mismatches 5; Indels
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Pred. No. 41;
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50.08;
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50.08;
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Best Local Similarity 50.0
Matches 5, Conservative
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Gaps

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A;Accession: A69950
A;Status: preliminary, nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Molecule type: DNA
A;Rosidues: 1-146 <KUN>
A;Cross-references: UNIPROT:P45945; GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14521.
A;Genetics:
A;Genetics:
A;Gene: yqcX
Query Match
Best Local Similarity 50.0%; Pred. No. 77;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EXEXPPRXXE 10

By BKEGFPREE 90
Search completed: October 26, 2004, 15:40:10
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Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).

Bukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Nipponbare;
Saeaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
clone:P0486G03.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 2; Length 262
Pred. No. 1.4e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki T., Matsumoto T., Yamamoto K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. InterPro; IPR003175; CDI.
Pfam; PF02234; CDI; 1.
Hypothetical protein.
SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;
                                                                                                                                                                                                                                                                                  Created)
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Q8F150
AAS69474
YQOZ CAEEL
Q8XSBZ
Q7QZA8
GR65_HUMAN
GR65_MOUSE
Q7XVIZ
GR65_RAT
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Hypothetical protein P0486G03.18.
Name=P0486G03.18;
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097460 oryza sativ

007831 oryza sativ

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Aas13375 glycine m
Q8gt29 lycopersico
Q9fb5 arabidopsis
Q6c915 yarrowia li
Q72u04 leptospira
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                                                                                  , Search time 55.7692 Seconds (without alignments) 103.171 Million cell updates/sec
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             5.1.6
Compugen Ltd.
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             GenCore version (c) 1993 - 2004
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SPN6_SCHPO
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Q6T2Z2
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Q8GT28
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Q6C915
Q72U04
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seg length: 200000000
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Nakamura Y., "Sequence "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2004 (TERMBLES) 77, Last sequence update)
10-MAY-2004 (TERMBLES) 77, Last sequence update)
10-MAY-2004 (TERMBLES) 27, Last annotation update)
6.001in-dependent kinase inhibitor 2;2 (Fragment).
6.1020 max (Soybean).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-07-2004 (TrEMBLrel. 27, Last annotation update)
Similarity to cyclin-dependent kinase inhibitor protein (Cyclin-dependent kinase inhibitor 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 25; DB 2; Length 166; llarity 50.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 5; Indels
                                                                                                                               Length 166;
                                                                                                                        Query Match 78.1%; Score 25; DB 2; Length 166 Best Local Similarity 50.0%; Pred. No. 1.6e+02; Matches 5; Indels Matches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Li S., Reverdatto S., Nielsen N.C.;
Lio S., Reverdatto S., Nielsen N.C.;
"CDNA of cell-cycle genes in Soybean cotyledons.";
Submitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY439104; AAS13377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin, Kinase.
NON TER 166
SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;
                                                                166
18850 MW; 40FB19CF72A8A640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                166 AA
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10-MAY-2004 (TrEMBLrel. 27, Last seg
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MEDLINE=20277480; PubMed=10819329;
InterPro; IPR003175; CDI.
Pfam; PF02234; CDI; 1.
Cyclin; Kinase.
NON TER 166 166
SEQÜENCE 166 AA; 18850
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DNA Res. 7:131-135(2000).
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AAS13377;
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max (Soybean).

Glycine max (Soybean).

Spermatophyta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

NCBI_TaxID=3847;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
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                                                                                    Score 26; DB 2; Length 262;
Pred, No. 1.4e+02;
0; Mismatches 5; Indels
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Pred. No. 60;
0; Mismatches 5; Indels
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Li S., Reverdatto S., Nielsen N.C.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY433174; AAS13377.1; -.
GO; GO:0016301; F:kinase activity; IEA.
                             l protein.
262 AA; 27138 MW; 42EC85C8276C0726 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome, Hypothetical protein.
SEQUENCE 62 AA; 7230 MW; 6BD1E040146CFAD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein TP0490.
OrderedLocusNames=TP0490;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
cyclin-dependent kinase inhibitor 2,2 (Fragment).
                                                                                                                                                                                                                                                                                                                        62 AA
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STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 281.375-388(1998).
EMBL; AE001225; AAC65477.1; -.
PIR; B71318; B71318.
TIGR, TP0490; -.
      EMBL; AP005002; BAD17213.1; -.
                                                                                       81.2%;
50.0%;
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illarity 50.0%;
Conservative (
                                                                  Query Match
Best Local Similarity 50...
Associated Similarity 50...
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                         1 EXEXFFXXXE 10
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es 5; Conserv
                      Hypothetical
SEQUENCE 26
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Q6T2Z0;
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Matches
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083503
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor 1;1.
Glycine max (Soybean).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, euroaids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photobaccerium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                             78.1%; Score 25; DB 2; Length 205; 50.0%; Pred. No. 2e+02; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.1%; Score 25; DB 2; Length 205; 50.0%; Pred. No. 2e+02;
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                                                                                                                                                                    Li S., Reverdatto S., Nielsen N.C.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; Av433101; AAS13374.1; -. GO; GO:0016301; F:kinase activity; IEA. InterPro; IPR003175; CDI. Pfan: PFro; IPR003175; CDI. Cyclin; Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Li S., Reverdatto S., Nielsen N.C.;
"CDNa of cell-cycle genes in soybean cotyledons.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBU databases.
EMBL; AY439101; AAS13374.1; --
                                                                                                                                                                                                                                                                                               205 AA; 22875 MW; 1B6F2D481710205E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA; 22875 MW; 1B6F2D481710205E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein YCAQ.
Name=YCAQ: OrderedLocusNames=PBPRB0166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          1 EXEXFFXXXE 10
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tes 5; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                     SEQUENCE FROM N.A.
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AAS13374;
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Q6LLB0
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                                                                                                                                  Arabidopsis.", p. 17163-1668(2001).

EMBL, AB028609 BAB02891.1; -..

EMBL, AJ301556; CAC41619.1; -..

GO, GO:0005534; C:nucleus; IEA.

GO; GO:0004661; F:cyclin-dependent protein kinase inhibitor a...

GO; GO:0007050; P:kinase activity; IEA.

InterPro; IPR03775; CDI.

Fran; PF02234; CDI; CDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Axillary Dud;
Shimiar-Sato S., Mori H.,
Shimiar-Sato S., Mori H.,
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029483; BAB20860.1; ...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:007060; P:cell cycle arrest; IEA.
Interbro; IPR03175; CDI.
                                                                                de Veylder L., Beeckman T., Beemster G.T.S., Krols L., Terras F
Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.;
"Functional analysis of Cyclin-dependent kinase inhibitors of
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                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 2; Length 185
Pred. No. 1.96+02;
5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.1%; Score 25; DB 2; Length 192
larity 50.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 5; Indels
           Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                     189 AA; 21424 MW; A66041310E8DDED6 CRC64;
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Last annotation update)
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Last sequence update)
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                                             SEQUENCE FROM N.A.
MEDLINE=21342510; PubMed=11449057;
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                                                                                                                                                                                                                                                                                                                                                                          78.1%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Matches 5, Conserv
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Q9FS28;
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

B SEQUENCE FROM N.A.

C SUDMITCE (MAY 2003) to the EMBL/Genbank/DDBJ databases.

EMBL; AE017104; AAP$4233.1; -.

EMBL; AE017104; AAP$4233.1; -.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0006861; F:cyclin-dependent protein kinase inhibitor a...;

R GO; GO:0007630; F:cyclin-dependent protein kinase inhibitor a...;

R GO; GO:0007630; F:cell cycle arrest; IEA.

R InterPro; IPR003175; CDI.

R Pfam; PF02234; CDI; 1.

M CYCLIN; Kinase.

M CYCLIN; Kinase.
             [1]
SEQUENCE FROM N.A.
The Rice Chromosome 10 Sequencing Consortium;
In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                     78.1%; Score 25; DB 2; Length 242;
50.0%; Pred. No. 2.46+02;
cive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                             242 AA; 26750 MW; F215A01234735928 CRC64;
                                                                                Science 300:1566-1569(2003)
                                                                                                                                                                                                                                                                                                                                    5; Conservative
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Matches 5; Conserv
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les 5; Conserv
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                                                                   chromosome 10.
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Matches 5
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Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
Valle G.;
                                                    Genome analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome Analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro
Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
05-Maranes-OSANBO-08pendent Kinase inhibitor.
07-yza sativa (japonica cultivar-group).
07-yza sativa (japonica cultivar-group).
07-yza sativa (japonica cultivar-group).
07-yza sativa Magnoliophyta; Liliopsida; Poales; Poaceae;
07-yza-29947;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Photobacterium.
                                                                                                                                                  Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 223;
                                                                high pressure adaptations."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL/. CR378675; CAG22039.1; Complete proteome; Hypothetical protein. SEQUENCE 223 AA; 25756 MW; FIDC29298B9C9C57 CRC64;
                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIL CESTAIN A.;
CESTAIN A.;
CESTAIN A.;
Submitted (MAR-2004) to the Embuloum
EMBL; CR378675; CAG22039.1; -.
Hypothetical protein.
Thypothetical protein.
Thypothetical Protein.
Thypothetical Protein.
Thypothetical Protein.
Thypothetical Protein.
Thypothetical Protein.
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10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein YCAQ.
                                                                                                                                                  78.1%; Score 25; DB 2; I
50.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 2; 1
Pred. No. 2.2e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                        223 AA
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                                                                                                                                                                              0: Mismatches
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                    Query Match
Best Local Similarity 50.0.
S; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0-
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                    189 EKETFFTALE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKETFFTALE 198
                                                                                                                                                                                                          1 EXEXPEXXXE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXEXFFXXXE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=74109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SS9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valle G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                      CAG22039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7XDH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7XDH8
                                                                                                                                                                                                                                                                          RESULT 11
CAG22039
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Submitted (OCT-2000) to the EWBL/GenBank/DDBJ databases.
BMBL; AC063145; AAG16867.1; -
Gramene; O9FW65; -
GO; OCO0005634; C:nucleus; IEA.
GO; GO:0004861; F::vglin-dependent protein kinase inhibitor a. . .; IEA.
GO; GO:0007860]; F:kinase activity; IEA.
GO; GO:0007050; F:call cycle arrest; IEA.
InterPro; IPR003175; CDI.
PEam; PF02234; CDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M., Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.1%; Score 25; DB 2; Length 242; 50.0%; Pred. No. 2.4e+02; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 AA; 26750 MW; F215A01234735928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 1-0CT-2003 (TrEMBLrel. 25, Last annotation update) Putative cyclin-dependent kinase inhibitor. Name-OSJNBD0094K03.16;
                                                                                                                                                                                                                                                                                        242 AA.
                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                        PRT;
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Search completed: October 26, 2004, 15:39:29
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                                                                                NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                         Deline_104;

WEDLINE_21368234; PubMed=11474104;

Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,

Galibert F., Finan T.M., Long S.R., Puehler A., Boistard P., Bothe G.,

Barloy-Hubler F., Barnett M.J., Becker A., Boistard D., Chain F.,

Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,

Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,

Hernandez-Luces I., Hong A., Hulzar L., Hyman R.W., Jones T., Kahn D.,

Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,

Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,

Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,

Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;

Fine composite genome of the legume symbiont Sinorhizobium mellioti.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 25; DB 2; Length 293; 50.0%; Pred. No. 2.9e+02; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 AA; 32763 MW; BF6530C41BF9245A CRC64;
                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
OrderedLocusNames=R00725; ORFNames=SM000780;
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Septin homolog spn6.
Namesepn6; ORFNames=SPCC188.12, SPCC584.09;
                                                                                  293 AA
                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LysR substrate; 1.
PROSITE; PS50931; HTH_LYSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EXEXPEXXXE 10
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                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
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SEQUENCE 293 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=382;
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ID SPN6_SCHPO
AC Q09883;
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                                                                                  092RW5
                                                                                                        Q92RW5
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Matches
                                         RESULT 14
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STEALNIS-218 Who was a standard of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AL032824; CAB37422.1; -...

EMBL, AL049662; CAB41232.1; -...

PIR; 741191; S62523.

GenebB. Spombe, SPCC188.12; -...

InterPro; IRR00038; GTP_Cell_Div.

Prodom; PD00256; GTP_Coll_Div.

Prodom; PD00256; GTP_Cell_Div.

Cell division; Coiled_coil; GTP-binding; Sporulation.

W BIND

37

44

GTP_(Potential).

DOMAIN

SEQUENCE 380 AA; 44011 MW; 450D86AEBEC2BCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu J.-Q., Pringle J.R.;
Submitted (MAR-2001) to Swiss-Prot.
-!. FUNCTION: Sporulation specific protein.
-!- SUBCELLUIAR LOCATION: Corrices of developing spores.
-!- SIMILARITY: Belongs to the septin family.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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Best Local Similarity 50.0
Matches 5; Conservative
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Job time : 57.7692 secs